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54 **Prevention of Bt resistance development.**

57 Plants made resistant to insects by transforming their nuclear genome with two or more DNA sequences, each encoding a different non-competitively binding B. thuringiensis protoxin or insecticidal part thereof, preferably the toxin thereof.

PREVENTION OF Bt RESISTANCE DEVELOPMENT

This invention relates to plant cells and plants, the genomes of which are transformed to contain at least two genes, each coding for a different non-competitively binding Bacillus thuringiensis ("B.thuringiensis" or "Bt") insecticidal crystal protein ("ICP") for a specific target insect species, preferably belonging to the order of Lepidoptera or Coleoptera. Such transformed plants have advantages over plants transformed with a single B. thuringiensis ICP gene, especially with respect to the prevention of resistance development in the target insect species against the at least two B. thuringiensis ICPs, expressed in such plants.

This invention also relates to a process for the production of such transgenic plants, taking into account the competitive and non-competitive binding properties of the at least two B. thuringiensis ICPs in the target insect species' midgut. Simultaneous expression in plants of the at least two genes, each coding for a different non-competitively binding B. thuringiensis ICP in plants, is particularly useful to prevent or delay resistance development of insects against the at least two B. thuringiensis ICPs expressed in the plants.

This invention further relates to a process for the construction of novel plant expression vectors and to the novel plant expression vectors themselves, which contain at least two B. thuringiensis ICP genes encoding at least two non-competitively binding B. thuringiensis ICPs. Such vectors allow integration and coordinate expression of the at least two B. thuringiensis ICP genes in plants.

BACKGROUND OF THE INVENTION

Since the development and the widespread use of chemical insecticides, the occurrence of resistant insect strains has been an important problem. Development of insecticide resistance is a phenomenon dependent on biochemical, physiological, genetic and ecological mechanisms. Currently, insect resistance has been reported against all major classes of chemical insecticides including chlorinated hydrocarbons, organophosphates, carbamates, and pyrethroid compounds (Brattsten et al., 1986).

In contrast to the rapid development of insect resistance to synthetic insecticides, development of insect resistance to bacterial insecticides such as B. thuringiensis sprays has evolved slowly despite many years of use (Brattsten et al., 1986). The spore forming gram-positive bacterium B. thuringiensis produces a parasporal crystal which is composed of crystal proteins (ICPs) having insecticidal activity. Important factors decreasing the probability of emergence of resistant insect strains in the field against B. thuringiensis sprays are firstly the short half life of B. thuringiensis after foliar application, secondly the fact that commercial B. thuringiensis preparations often consist of a mixture of several insecticidal factors including spores, ICP(s) and eventually beta-exotoxin (Shields, 1987) and thirdly the transitory nature of plant-pest interactions. Many successful field trials have shown that commercial preparations of B. thuringiensis containing the spore-crystal complex, effectively control lepidopterous pests in agriculture and forestry (Krieg and Langenbruch, 1981). B. thuringiensis is at present the most widely used pathogen for microbial control of insect pests. Various laboratory studies in which selection against B. thuringiensis was applied over several generations of insects have confirmed that resistance against B. thuringiensis is seldom obtained. However, it should be emphasized that the laboratory conditions represented rather low selection pressure conditions (cfr.infra).

For example, Goldman et al. (1986) have applied selection with B. thuringiensis israelensis toxin over 14 generations of Aedes aegypti and found only a marginal decrease in sensitivity. The lack of any observable trend toward decreasing susceptibility in the selected strains may be a reflection of the low selection pressure (LC_{50}) carried out over a limited number of generations. However, it should be pointed out that Georgiou et al. (In : Insecticide Resistance in Mosquitoes : Research on new chemicals and techniques for management. In "Mosquito Control Research, Annual Report 1983, University of California.") with Culex quinquefasciatus obtained an 11-fold increase in resistance to B. thuringiensis israelensis after 32 generations at LC_{95} selection pressure.

McGaughey (1985) reported that the grain storage pest Plodia interpunctella developed resistance to the spore-crystal complex of B. thuringiensis : after 15 generations of selection with the Indian meal moth, Plodia interpunctella, using a commercial B. thuringiensis preparation (HD-1, Dipel, Abbott Laboratories, North Chicago, Illinois 60064, USA) a 100 times decrease in B. thuringiensis sensitivity was reported. Each of the colonies was cultured for several generations on a diet treated with a constant B. thuringiensis dosage which was expected to produce 70-90% larval mortality. Under these (high selection pressure) conditions insect resistance to B. thuringiensis progressed rapidly. More recently, development of resistance against B. thuringiensis is also reported for the almond moth, Cadra cautella (McGaughey and

Beeman, 1988). Resistance was stable when selection was discontinued and was inherited as a recessive trait (McGaughey and Beeman, 1988). The mechanism of insect resistance to B. thuringiensis toxins of Plodia interpunctella and Cadra cautella has not been elucidated. The main cause of B. thuringiensis resistance development in both cases were the environmental conditions prevailing during grain storage.

5 Under these conditions the environment is relatively stable, so B. thuringiensis degradation is slow and permits successive generations of the pest to breed in the continuous presence of the microbial insecticide. The speed at which Plodia developed resistance to B. thuringiensis in this study, suggests that it could do so within one single storage season in the bins of treated grain.

Although insect resistance development against B. thuringiensis has mostly been observed in laboratory and pilot scale studies, very recent indications of B. thuringiensis resistance development in Plutella xylostella populations in the (cabbage) field have been reported (Kirsch and Schmutterer, 1988). A number of factors have led a continuous exposure of P. xylostella to B. thuringiensis in a relatively small geographic area. This and the short generation cycle of P. xylostella have seemingly led to an enormous selection pressure resulting in decreased susceptibility and increased resistance to B. thuringiensis.

15 A procedure for expressing a B. thuringiensis ICP gene in plants in order to render the plants insect-resistant (EP patent publication 0193259 [which is incorporated herein by reference]; Vaeck et al., 1987; Barton et al., 1987; Fischhoff et al., 1987) provides an entirely new approach to insect control in agriculture which is at the same time safe, environmentally attractive and cost-effective. An important determinant for the success of this approach will be whether insects will be able to develop resistance to B. thuringiensis ICPs expressed in transgenic plants (Vaeck et al., 1987; Barton et al., 1987; Fischhoff et al., 1987). In contrast with a foliar application after which B. thuringiensis ICPs are rapidly degraded, the transgenic plants will exert a continuous selection pressure. It is clear from laboratory selection experiments that a continuous selection pressure has led to adaptation to B. thuringiensis and B. thuringiensis components in several insect species (cfr. supra). In this regard, it should be pointed out that the conditions in the laboratory which resulted in the development of insect-resistance to B. thuringiensis are very well comparable to the situation in transgenic plants which will produce B. thuringiensis ICPs and provide a continuous selection pressure on insect populations feeding on said plants. Mathematical models of selection pressure predict that if engineered insect-resistant plants become a permanent part of their environment, resistance development in insects will emerge rapidly (Gould, 1988). Thus the chances for the development of insect resistance to B. thuringiensis in transgenic plants may be considerably increased as compared to the field application of B. thuringiensis sprays. A Heliothis virescens strain has been reported that is 20 x resistant to B. thuringiensis HD-1 ICP produced by transgenic Pseudomonas fluorescens and 6x resistant to pure ICP (Stone et al., 1989). Furthermore, the monetary and human costs of resistance are difficult to assess, but loss of pesticide effectiveness invariably entails increased application frequencies and dosages and, finally, more expensive replacement compounds, as new pesticides become more difficult to discover and develop. Therefore it is desirable to develop strategies that can greatly delay or prevent the evolution of resistance to B. thuringiensis.

B. thuringiensis strains active against Lepidoptera (Dulmage et al., 1981), Diptera (Goldberg and Margalit, 1977) and Coleoptera (Krieg et al., 1983) have been described. It has become clear from various publications that there is a substantial heterogeneity among ICPs from different strains active against Lepidoptera as well as among ICPs from strains active against Coleoptera. An overview of the different B. thuringiensis ICP genes that have been characterized is given in table 1.

Most of the anti-Lepidopteran crystal protein genes encode 130 to 140 kDa protoxins which dissolve in the alkaline environment of the insect midgut and are proteolytically activated into an active toxin of 60-65 kDa. (Bt3, Bt2, Bt73, Bt14, Bt15, Bt4, Bt18). All these toxins are related and can be recognized as members of the same family based on sequence homologies, the sequence divergence however is substantial and also the insecticidal spectrum among the order Lepidoptera may be substantially different (Höfte et al., 1988).

The P2 toxin gene and the cry B2 gene are more divergent from the above mentioned genes in that they do not encode high molecular weight protoxins but rather toxins of around 70 kDa (Donovan et al., 1988; Widner and Whiteley, 1989, respectively).

It has recently become clear that heterogeneity exists also in the anti-Coleopteran toxin gene family. Whereas several previously reported toxin gene sequences from different B. thuringiensis isolates with anti-Coleopteran activity were identical (European patent ("EP") publications 0149162 and 0202739), the sequences and structure of bt21 and bt22 are substantially divergent (EP patent application n° 89400428.2).

While the insecticidal spectra of ICPs are different, the major pathway of their toxic action is believed to be common. All B. thuringiensis ICPs, for which the mechanism of action has been studied in any detail,

interact with the midgut epithelium of sensitive species and cause lysis of the epithelial cells (Knowles and Ellar, 1986) due to the fact that the permeability characteristics of the brush border membrane and the osmotic balance over this membrane are perturbed. In the pathway of toxic action of B. thuringiensis ICPs, the binding of the toxin to receptor sites on the brush border membrane of these cells is an important feature (Hofmann et al., 1988b). The toxin binding sites in the midgut can be regarded as an ICP-receptor since toxin is bound in a saturable way and with high affinity (Hofmann et al., 1988a).

Although this outline of the mode of action of ICPs is generally accepted, it remains a matter of discussion what the essential determinant(s) are for the differences in their insecticidal spectra. Haider et al. (1986) emphasize the importance of specific proteases in the insect midgut. Hofmann et al. (1988b) indicate that receptor binding is a prerequisite for toxic activity and describe that Pieris brassicae has two distinct receptor populations for two toxins. Other authors have suggested that differences in the environment of the midgut (e.g. pH of the midgut) might be crucial.

15 SUMMARY OF THE INVENTION

In accordance with this invention, a plant is provided having, stably integrated into its genome, at least two B. thuringiensis ICP genes, encoding at least two non-competitively binding insecticidal B. thuringiensis ICPs, preferably the active toxins thereof, against a specific target insect, preferably against Lepidoptera or Coleoptera. Such a plant is characterized by the simultaneous expression of the at least two non-competitively binding B. thuringiensis ICPs.

Also in accordance with this invention, at least two ICP genes, particularly two genes or parts thereof coding for two non-competitively binding anti-Lepidopteran or anti-Coleopteran B. thuringiensis ICPs, are cloned into a plant expression vector. Plant cells transformed with this vector are characterized by the simultaneous expression of the at least two B. thuringiensis ICP genes. The resulting transformed plant cell can be used to produce a transformed plant in which the plant cells: 1) contain the at least two B. thuringiensis ICP genes or parts thereof encoding at least two non-competitively binding anti-Lepidopteran or anti-Coleopteran B. thuringiensis ICPs as a stable insert into their genome; and 2) express the genes simultaneously, thereby conferring on the plant improved insect resistance which is particularly useful to prevent or delay development of resistance to B. thuringiensis of insects feeding on the transformed plant.

Further in accordance with this invention, plant expression vectors are provided which allow integration and simultaneous expression of at least two ICP genes in a plant cell and which comprise one or more chimeric genes, each containing in the same transcriptional unit: a promoter which functions in plant cells to direct the synthesis of mRNA molecules; one or more different ICP genes each encoding a non-competitively binding B. thuringiensis ICP; preferably a marker gene; a 3' non-translated DNA sequence which functions in plant cells for 3' end formation and the addition of polyadenylate nucleotides to the 3' end of the mRNA sequence; and optionally a DNA sequence encoding a protease-sensitive protein part between any two ICP genes.

40 DETAILED DESCRIPTION OF THE INVENTION

45 Definitions

As used herein, "ICP" should be understood as an intact protein or a part thereof which has insecticidal activity and which can be produced in nature by B. thuringiensis. An ICP can be a protoxin, as well as an active toxin or another insecticidal truncated part of a protoxin which need not be crystalline and which need not be a naturally occurring protein.

As used herein, "protoxin" should be understood as the primary translation product of a full-length gene encoding an ICP.

As used herein, "toxin", "toxic core" or "active toxin" should all be understood as a part of a protoxin which can be obtained by protease (e.g., by trypsin) cleavage and has insecticidal activity.

As used herein, "gene" should be understood as a naturally-occurring full-length DNA sequence encoding a protein, such as is found in nature, as well as a truncated fragment thereof encoding the active part of the protein encoded by the full-length DNA sequence.

As used herein, "truncated B. thuringiensis gene" should be understood as a fragment of a full-length B. thuringiensis gene which still encodes at least the toxic part of the B. thuringiensis ICP. preferentially the

toxin.

As used herein, "marker gene" should be understood as a gene encoding a selectable marker (e.g. encoding antibiotic resistance) or a screenable marker (e.g. encoding a gene product which allows the quantitative analysis of transgenic plants).

5 Two ICPs are said to be "competitively binding ICPs" for a given insect species when one ICP competes for all ICP receptors of the other ICP, which receptors are present in the brush border membrane of the midgut of the insect species.

Two ICPs are said to be "non-competitively binding ICPs" when, for at least one target insect species, the first ICP has at least one receptor for which the second ICP does not compete and the second ICP has
10 at least one receptor for which the first ICP does not compete, which receptors are present in the brush border membrane of the midgut of the insect species.

A "receptor" should be understood as a molecule which can bind to a ligand (here an B. thuringiensis ICP, preferably a toxin) with affinity (typically a dissociation constant (Kd) between 10^{-11} and 10^{-6} M) and saturability. A determination of whether two ICPs are competitively or non-competitively binding ICPs can
15 be made by determining whether: 1) a first ICP competes for all of the receptors of a second ICP when all the binding sites of the second ICP with an affinity in the range of about 10^{-11} to 10^{-6} M can be saturated with the first ICP in concentrations of the first ICP of about 10^{-5} M or less (e.g., down to about 10^{-11} M); and
2) the second ICP competes for all of the receptors of the first ICP when all the binding sites of the first ICP with an affinity in the range of about 10^{-11} to 10^{-6} M can be saturated with the second ICP in
20 concentrations of the second ICP of about 10^{-5} M or less.

General Procedures

25 This section describes in broad terms a general procedure for the evaluation and exploitation of at least two B. thuringiensis ICP genes for prevention of resistance development in insects against B. thuringiensis ICPs expressed in transgenic plants. A non-exhaustive list of consecutive steps in the experimental procedure is described, whereas particular examples which are based on this methodology and which illustrate the invention are given in the next section.

30 In accordance with this invention, the respective ICPs can be isolated in a conventional manner from the respective strains as listed in table 1. The ICPs can be used to prepare monoclonal or polyclonal antibodies specific for these ICPs in a conventional manner (Höfte et al., 1988).

The ICP genes can be isolated from their respective strains in a conventional manner. Preferably, the ICP genes are each identified by digesting total DNA from their respective strains with suitable restriction
35 enzyme(s); size fractionating the DNA fragments, so produced, into DNA fractions of 5 to 10 Kb; ligating such fractions to suitable cloning vectors e.g. pEcoR251, deposited at DSM under the provisions of the Budapest Treaty, accession number n° 4711 on July 13, 1988; transforming E. coli with the cloning vectors and screening the clones with a suitable DNA probe. The DNA probe can be constructed : 1) from a highly conserved region which is commonly present in different B. thuringiensis genes which encode crystal
40 protoxins against Coleoptera or Lepidoptera such as on the basis of the N-terminal amino acid sequence determined by gas-phase sequencing of the purified proteins (European patent application 88/402,115.5).

Alternatively, the desired fragments, prepared from total DNA of the respective strains, can be ligated in suitable expression vectors (e.g. a pUC vector, Yanisch-Perron et al., 1985, with the insert under control of the lac promoter) and transformed in E. coli, and the clones can then be screened by conventional colony
45 immunoprobng methods (French et al., 1986) for expression of the toxins with monoclonal or polyclonal antibodies raised against the toxins produced by said strains.

The isolated B. thuringiensis ICP genes can then be sequenced in a conventional manner according to procedures well-known in the art (e.g. Maxam and Gilbert, 1980).

At present, several ICP genes have been cloned from different subspecies of B. thuringiensis (table 1).
50 The nucleotide sequence from several of these B. thuringiensis ICP genes have been reported. Whereas several sequences are identical or nearly-identical and represent the same gene or slight variants of the same gene, several sequences display substantial heterogeneity and show the existence of different B. thuringiensis ICP gene classes. Several lines of evidence suggest that all these genes specify a family of related insecticidal proteins. Analysis of the distribution of B. thuringiensis ICPs in different B. thuringiensis strains by determination of the protein composition of B. thuringiensis crystals, by immunodetection using
55 polyclonal antisera or monoclonals against purified crystals, or by use of gene-specific probes, shows that subspecies of B. thuringiensis might contain up to three related B. thuringiensis ICP genes belonging to different classes (Kronstad et al., 1983).

To express the isolated and characterized gene in a heterologous host for purification and characterization of the recombinant protein, the organism of choice is preferentially Escherichia coli. A number of expression vectors for enhanced expression of heterologous genes in E. coli have been described (e.g. Remaut et al., 1981). Usually the gene is cloned under control of a strong regulatable promoter e.g. the
 5 lambda pL or pR promoters (e.g. Botterman and Zabeau, 1987), or the lac (e.g. Fuller, 1982) and tac (e.g. De Boer et al., 1983) promoters and provided with suitable translation initiation sites (e.g. Stanssens et al, 1985). Gene cassettes of the B. thuringiensis ICP genes can be generated by site directed mutagenesis, e.g. according to the procedure described by Stanssens et al., 1985. This allowed to create cassettes comprising for example truncated gene fragments encoding the toxin core fragment or hybrid genes with a
 10 selectable marker according to the procedures as described in patent application EP 88402241.9.

The cells of an E. coli culture, which has been induced to produce the recombinant ICPs, are harvested. The method to induce the cells to produce the recombinant toxin depends on the choice of the promoter (e.g. lac (Fuller, 1982) is induced by isopropyl-B-D-thiogalacto-pyranoside (IPTG); pL is induced by temperature shock (Bernard et al., 1979)). The recombinant ICP is usually deposited in the cells as
 15 insoluble inclusions (Hsuing and Becker, 1988). The cells are lysed to liberate the inclusions. The bulk of E. coli proteins is removed in subsequent washing steps. A semi-purified protoxin pellet is obtained, the protoxin can be dissolved in alkaline buffer (e.g. Na₂CO₃, pH 10). The procedure for Bt2, which is also applicable to other recombinant toxins, has been described by Höfte et al., 1986.

In accordance with this invention the binding of various toxins to ICP receptors on the brush border
 20 membrane of the columnar midgut epithelial cells of various insect species is investigated. The brush border membrane is the primary target of the toxin, and membrane vesicles preferentially derived from the brush border membrane can be obtained according to Wolfersberger et al., 1987.

The binding to ICP receptors of one or more ICPs (e.g., ICP A, ICP B, etc.) is usually characterized as follows (Hofmann et al, 1988b):

- 25 1. ICP A is labelled with a suitable marker (usually a radioisotope such as ¹²⁵I)
2. Brush border membranes are incubated with a small amount (preferably less than 10⁻¹² M) of labelled ICP A together with different concentrations of non-labelled ICP A (preferably from less than 10⁻¹¹ to 10⁻⁵ M)
3. For all concentrations tested the amount of labelled ICP A bound to the brush border membranes
 30 is measured.
4. Mathematical analysis of these data allows one to calculate various characteristics of the ICP receptor such as the magnitude of the population of binding sites (Scatchard, 1949).
5. Competition by other toxins (e.g. toxin B) is preferably studied by incubating the same amount of labelled ICP A with brush border membranes in combination with different amounts of ICP B (preferentially
 35 from 10⁻¹¹ to 10⁻⁵ M). Subsequently, steps 3 and 4 are repeated.

By this procedure, it has been found that Bt3 toxin, Bt2 toxin and Bt73 toxin are competitively binding anti-Lepidopteran ICPs for Manduca sexta and Heliothis virescens (see example 6). Various other combinations of toxins have been found to be non-competitively binding anti-Lepidopteran or anti-Coleopteran toxins (example 6). These combinations are given as examples and do not limit the scope of the invention.

40 Although, the concept of competitiveness versus non-competitiveness of ICP binding does not have any immediate practical importance by itself, the observation of the non-competitiveness of two B. thuringiensis ICPs active against the same target insect is of practical importance because such a combination of two non-competitively binding B. thuringiensis ICPs can be used to prevent resistance development of in the target insect against such B. thuringiensis ICPs. A selection experiment with M. sexta, using Bt2, Bt18, and a
 45 mixture of Bt2 and Bt18 toxins, has shown that Bt2 and Bt18 are two non-competitively binding anti-Lepidopteran toxins. After 20 generations of selection, a very pronounced reduction in ICP sensitivity was observed in the selection experiments with Bt2 or Bt18 alone (>100 times). The reduction in sensitivity in the selection experiment with a Bt2-Bt18 mixture was only marginal (3 times).

This demonstrates the unexpected advantage of a simultaneous use of two non-competitively binding
 50 ICPs, in a situation which models the high selection pressure which will exist with the use of transgenic plants. The two resistant strains selected respectively with Bt2 and Bt18 showed a specific loss in receptor sites for respectively Bt2 and Bt18 toxin. In each case, receptor sites for the toxin which was not used for selection were not affected or their concentration even increased. Thus, the Bt2 selected strain retained its Bt18 receptors, and the Bt18 selected strain developed an increased number of Bt2 receptors. Indeed, the
 55 Bt18 selected strain showed an increased sensitivity for Bt2 along with its increased Bt2 receptor concentration. No significant changes in receptor sites were found in the strain selected against the combined toxins. These findings are described in detail in example 7. This finding has immediate relevance to any combination of non-competitively binding anti-Lepidopteran or Coleopteran ICPs which will have the

same beneficial effect against their common target insects.

Such a combination, when directly expressed in the transgenic plant, will also offer the substantial advantage of reducing the chance for development of insect resistance against the *B. thuringiensis* ICPs expressed in the plant. There may be additional benefits because the combined spectrum of two toxins
 5 may be broader than the spectrum of a single ICP expressed in a plant (e.g. examples 8, 9 and 10).

If, among two competitively binding ICPs, one has a larger binding site population than the other against a given target insect, it will be most advantageous to use the one with the largest population of binding sites to control this target pest in a combination with the most suitable non-competitively binding *B. thuringiensis* ICP. For example, as described in example 6, it will be useful to use Bt73 against *Heliothis*
 10 *virescens* rather than Bt2 or Bt3, and it is preferred to use Bt3 against *Manduca sexta* rather than Bt2 or Bt73. The selected gene can then be combined with the best suitable non-competitively binding ICP.

Previously, plant transformations involved the introduction of a marker gene together with a single ICP gene, within the same plasmid, in the plant genome (e.g. Vaeck et al., 1987; Fischhoff et al., 1987). Chimeric ICP genes usually comprised either an intact ICP gene or a truncated ICP gene fragment encoding the toxin
 15 core or hybrid gene with a selectable marker gene such as *neo* coding for neomycin phosphotransferase. The chimeric ICP and any chimeric marker gene were between the T-DNA border repeats for *A. tumefaciens* Ti-plasmid mediated transformation.

This invention involves the combined expression of two or even more *B. thuringiensis* ICP genes in transgenic plants. The insecticidally effective *B. thuringiensis* ICP genes, which encode two non-competitively binding ICPs for a target insect species, preferably the respective truncated ICP genes, are inserted
 20 in a plant cell genome, preferably its nuclear genome, so that the inserted genes are downstream of, and under the control of, a promoter which can direct the expression of the genes in the plant cell. This is preferably accomplished by inserting in the plant cell genome one or more chimaeric genes, each containing in the same transcriptional unit: at least one ICP gene; preferably a marker gene; and optionally
 25 a DNA sequence encoding a protease (e.g., trypsin) sensitive or cleavable protein part between any two ICP genes in a chimaeric gene. Each chimaeric gene also contains a promoter which can direct the at least one ICP gene in the plant cell.

Preferred promoters for such chimaeric genes include: the strong constitutive 35S promoter obtained from the cauliflower mosaic virus, isolates CM 1841 (Gardner et al., 1981), CabbB-S (Franck et al., 1980)
 30 and CabbB-JI (Hull and Howell, 1987); and the TR1' promoter and the TR2' promoter which drive the expression of the 1' and 2' genes, respectively, of the T-DNA (Velten et al., 1984). Alternatively, a promoter can be utilized which is specific for one or more tissues or organs of the plant whereby the inserted genes are expressed only in cells of the specific tissue(s) or organ(s). Examples of such promoters are a stem-specific promoter such as the AdoMet-synthetase promoter (Peleman et al., 1989) or a seed-specific
 35 promoter such as the 2S promoter (Krebbers et al., 1988). For example, the genes could be selectively expressed in the leaves of a plant (e.g., potato) by placing the genes under the control of a light-inducible promoter such as the promoter of the ribulose-1,5-bisphosphate carboxylase small subunit gene of the plant itself or of another plant such as pea as disclosed in U.S. patent application 821,582 and European patent application 86/300, 291.1. Another alternative is to use a promoter whose expression is inducible (e.g. by
 40 temperature or chemical factors).

Finally, a 3' non-translated DNA sequence, which functions in plant cells for 3' end formation and the addition of polyadenylate nucleotides to the 3' end of the mRNA sequence encoded by the at least one ICP gene in the plant cell, also forms part of each of such chimeric genes. Examples are the 3' untranslated end of the octopine synthase gene, the nopaline synthase gene and the T-DNA gene 7 (Velten and Schell,
 45 1985).

Using *A. tumefaciens* Ti vector-mediated transformation methodology, all chimeric genes are between the T-DNA border repeats of suitable disarmed Ti-plasmid vectors (Deblaere et al., 1988). The chimeric genes can also be in non-specific plasmid vectors which can be used for direct gene transfer (e.g. as described by Pazkowski et al., 1984; De La Pena et al., 1986). Different strategies can be followed to obtain
 50 a combined expression of two *B.thuringiensis* ICP genes in transgenic plants as summarized below:

I Chimeric gene constructs whereby two or more ICP genes and a marker gene are transferred to the plant genome as a single piece of DNA and lead to the insertion in a single locus in the genome

la The genes can be engineered in different transcriptional units each under control of a distinct promoter

To express two or more ICP genes and a marker gene as separate transcriptional units, several promoter fragments directing expression in plant cells, can be used as mentioned earlier. All combinations of these promoters mentioned above in the chimaeric constructs for one ICP gene are possible. Examples of such individual chimeric constructs are described for the bt2 gene in EP patent publication EP 0193259, for the bt13 gene in EP patent application n° 88402115.5 and for the bt18 gene in EP patent application n° 88402241.9. The ICP genes in the chimeric genes of this invention can be the intact ICP gene or a truncated gene fragment encoding the toxic core of the ICP. The individual chimeric genes are cloned in the same plasmid vector according to standard procedures.

1b Two genes (e.g., either an ICP and a marker gene or two ICP genes) or more can be combined in the same transcriptional unit

To express two or more ICP genes in the same transcriptional unit, the following cases can be distinguished:

In a first case, hybrid genes in which the coding region of one gene is in frame fused with the coding region of another gene can be placed under the control of a single promoter. Fusions can be made between either an ICP and a marker gene or between two ICP genes. An example of an ICP gene-marker gene fusion has been described in EP patent publication 0193259, i.e. a hybrid bt2-neo gene encoding a Bt2-NPTII fusion protein was used.

Another possibility is the fusion of two ICP genes. Between the genes, each encoding an ICP which still is insecticidally active (i.e., a toxic part of the protoxin), a gene fragment encoding a protease (e.g., trypsin) sensitive protein part should be included, such as a gene fragment encoding a part of the N-terminal or C-terminal amino acid sequence of one of the ICPs which is removed or cleaved upon activation by the midgut enzymes of the target insect species.

In a second case, the coding regions of the respective genes can be combined in dicistronic units placed under the control of a promoter. The coding regions of the two ICP genes are placed after each other with an intergenic sequence of defined length. A single messenger RNA molecule is generated leading to the translation into two separate gene products. Based on the modified scanning model (Kozak, 1987), the concept of reinitiation of translation has been accepted provided that a termination codon in frame with the upstream ATG precedes the downstream ATG. Experimental also demonstrated that the plant translational machinery is able to synthesize several polypeptides from a polycistronic mRNA (Angenon et al., in preparation).

II Chimeric constructs with one or more ICP genes that are transferred to the genome of a plant already transformed with a one or more ICP genes

Several genes can be introduced into a plant cell during sequential transformation steps (retransformation) if an alternative system to select transformants is available for the second round of transformation. This retransformation leads to the combined expression of ICP genes which are introduced at multiple loci in the genome. Preferably two different selectable marker genes will be used in the two consecutive transformation steps. The first marker will be used for selection of transformed cells in the first transformation, while the second marker is used for selection of transformants in the second round of transformation. Sequential transformation steps using kanamycin and hygromycin have been described for example by Sandler et al., 1988 and Delauney et al., 1988.

III Chimeric constructs with one or more ICP genes, that are separately transferred to the nuclear genome of separate plants in independent transformation events and are subsequently combined in a single plant genome through crosses.

The first plant should be a plant transformed with a first ICP gene or an F1 plant derived herefrom through selfing (preferably an F1 plant which is homozygous for the ICP gene). The second plant should be a plant transformed with a second ICP gene or an F1 plant derived herefrom through selfing (preferably an F1 plant which is homozygous for the second ICP gene). Selection methods can be applied to the plants obtained from this cross in order to select those plants having the two ICP genes present in their genome (e.g. Southern blotting) and expressing the two ICPs (e.g. separate ELISA detection of the immunologically

different ICPs).

In particular this will be a useful strategy to produce hybrid varieties from two parental lines transformed with a different ICP gene as well as to produce inbred lines containing two different ICP genes through crossing of two independent transformants (or their F1 selfed offspring) from the same inbred line.

5

IV Chimeric constructs with one or more ICP genes separately transferred to the genome of a single plant in the same transformation experiment leading to the insertion of the respective chimeric genes at multiple loci.

10

Cotransformation consists in the simultaneous transformation of a plant with two different expression vectors, one containing the first ICP gene, the second one containing the second ICP gene. Along with each ICP gene, a different marker gene may be used and selection can be applied with the two markers simultaneously. Alternatively a single marker can be used and a sufficiently large number of selected plants can be screened again in order to find those plants having the two ICP genes (e.g. by Southern blotting) and expressing the two proteins (e.g. by means of ELISA). Cotransformation with more than one T-DNA has been accomplished by using simultaneously two different strains of *Agrobacterium*, each with a different Ti-plasmid (Depicker et al., 1985) or with one strain of *Agrobacterium* containing two T-DNAs on separate plasmids (de Framond et al., 1986). Direct gene transfer using a mixture of two plasmids has been used to cotransform plant cells with a selectable and a non-selectable gene (Schocher et al., 1986).

Transgenic plants obtained can be used in further plant breeding schemes. The transformed plant can be selfed to obtain a plant which is homozygous for the inserted genes. If the plant is an inbred line this homozygous plant can be used to produce seeds directly or as a parental line for a hybrid variety. The gene can also be crossed into open pollinated populations or other inbred lines of the same plant using conventional plant breeding approaches.

It is obvious that other plant transformation methods can be used and are within the scope of the invention as long as the result is a plant which expresses two or more non-competitively binding ICPs. Needless to say, this invention is not limited to the use of *Agrobacterium tumefaciens* Ti-plasmids for transforming plant cells with ICP genes encoding such non-competitively binding ICPs. Other known methods for plant cell transformation such as by electroporation or vector systems based on plant viruses or pollen, can be used for transforming monocotyledonous and dicotyledonous plants in order to obtain plants, which express two non-competitively binding ICPs. Furthermore, DNA sequences encoding two non-competitively binding ICPs other than those disclosed herein can be used for transforming plants. It will be clear to those skilled in the art that each of the ICP genes can be encoded by equivalent DNA sequences, taking into consideration the degeneration of the genetic code. Also, ICPs with only few amino-acid changes obtained through mutations in the ICP gene could still encode a protein with essentially the same characteristics (e.g. insecticidal activity, receptor binding).

The following examples illustrate the invention and are not intended to limit its scope. Those skilled in the art will recognize that other combinations of two or more non-competitively binding *B. thuringiensis* ICP genes can be used to transform plants in order to prevent the development in a target insect of resistance against *B. thuringiensis* ICPs expressed in transgenic plants and that equivalent embodiments are included herein. All procedures for making and manipulating DNA were carried out by the standardized procedures described in Maniatis et al, Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory (1982).

45

EXAMPLE 1: Collection of genes

The collection of anti-Lepidopteran and anti-Coleopteran Bt genes encoding ICPs, which are the subject of the examples, is described in table 1. References for the respective genes are indicated. The origin, the isolation and characterization of the Bt genes, which have not been published, are described below. Bt strains, such as strains HD-68, HD-110, and HD-73, are publicly available from the Agricultural Research Culture Collection, Northern Region Research Center, North University, Peoria, Illinois 61604, U.S.A.

55

b13 gene:

From *B. thuringiensis* var. *aizawai* HD-68 a ICP gene was cloned. Characterization of this gene revealed

an open reading frame of 3528 bp which encodes a protoxin of 133 kDa. This gene was identical to the one described by Schnepf et al., 1985.

5 bt4 gene:

A genomic library was prepared from total DNA of strain B. thuringiensis aizawai HD-68. Using the 1.1 kb internal HindIII fragment of bt2 as a probe, a gene designated bt4 was isolated. Characterization of this gene revealed an open reading frame of 3495 bp which encodes a protoxin of 132 kDa and a trypsin
10 activated toxin fragment of 60 kDa. This (insect controlling protein) gene differs from previously identified genes and was also found in several other strains of subspecies aizawai and entomocidus including HD-110. Fig. 13 shows the nucleotide sequence and deduced amino acid sequence of the open reading frame ("ORF") of the bt4 gene extending from nucleotide 264 to nucleotide 3761.

15

bt14 and bt15 genes:

A genomic library was prepared from total DNA of strain B. thuringiensis var. entomocidus HD-110 by partial Sau3A digest of the total DNA and cloning in the vector pEcoR251, deposited at DSM under the
20 provisions of the Budapest Treaty, accession number n° 4711 on July 13, 1988. Using monoclonal antibodies (Höfte et al., 1988), at least three structurally distinct ICPs were identified in crystals of B. thuringiensis entomocidus HD-110. These monoclonal antibodies were used to clone the three different ICP genes from this B. thuringiensis strain. One of these genes is the bt4 gene as described above.

The second gene was called "bt15". Fig. 14 shows the nucleotide sequence and deduced amino acid
25 sequence of the ORF of the bt15 gene, isolated from HD-110, extending from nucleotide 234 to nucleotide 3803. The Shine and Dalgarno sequence, preceding the initiation codon is underlined. This gene has an open reading frame of 3567 bp which encodes a protoxin of 135 kDa and a 63 kDa toxin fragment. A similar gene has been described by Honnee et al. 1988, isolated from B. thuringiensis entomocidus 60.5. The bt15 gene differs from the published sequence at three positions : an Ala codon (GCA) is present instead of an
30 Arg codon (CGA) at position 925 and a consecution of a Thr-His codon (ACGCAT) is present instead of a Thr-Asp codon (ACGGAT) at position 1400. The numbers of the positions are according to Honnee et al., 1988. Another similar gene has been described by Sanchis et al. (EP publication 0295156), isolated from B. thuringiensis aizawai 7-29 and entomocidus 6-01. The bt15 gene is different from this published nucleotide
35 sequence at three different places : 1) a Glu codon (GAA) instead of an Ala codon (GCA) at position 700; 2) the sequence TGG, CCA, GCG, CCA instead of TGC, CAG, CGC, CAC, CAT at position 1456 and 3) an Arg codon (CGT) instead of an Ala codon (GCG) at position 2654. The numbers of the positions are according to Sanchis et al (EP publication 0295156).

The third gene isolated was called "bt14". It has an open reading frame of 3621 bp which encodes a 137
40 kDa protoxin and a 66 kDa activated toxin fragment. A similar gene has been cloned from B. thuringiensis HD-2 (Brizzard and Whiteley, 1988). The bt14 gene differs from the published nucleotide sequence by two nucleotide substitutions : a T instead of a C at position 126, and a C instead of a T at position 448. In the first case, the Ile codon (ATT or ATC) is conserved whereas in the second case the Tyr codon (TAT) is converted to a His codon (CAC). The numbers of the positions are according to Brizzard and Whiteley (1988).

45

bt2 gene:

Cloning of the bt2 gene is described in EP publication 0193259.

50 Cloning of the bt18 gene was performed as described in EP application n° 88402241.9.

bt13 gene:

55 The bt13 gene was cloned as described in EP application n° 88402115.5.

bt21 and bt22 genes:

both genes, encoding Coleopteran-active ICPs, were cloned as described in EP application n° 89400428.2.

5 EXAMPLE 2 : construction of gene cassettes and expression of bt genes in E.coli

1) bt2, bt18: the construction of bt2 and bt18 gene cassettes has been described in previous EP patent applications n° 86300291.1 and 88402241.9 respectively. Basically, they comprise a truncated gene encoding the toxin core fragment and a hybrid gene consisting of the toxin core fragment in frame fused to the N-terminus of the neo gene.

10 2) bt14, bt15: as described in EP application n° 88402241.9, gene cassettes for the bt14 and bt15 genes respectively were designed in order to express the genes in E.coli and in plants. First, a NcoI site was introduced at the N-terminus of the genes by site mutagenesis. In the case of the bt15 gene, the substitution of the TT nucleotides immediately in front of the ATG codon into CC yielded a NcoI site overlapping with the ATG initiation codon. This site was introduced using the pMa/c vectors for site directed mutagenesis (Stanssens et al., 1987) and a 28-mer oligonucleotide with the following sequence:
15 5'-CGGAGGTATTCCATGGAGGAAAATAATC-3'. This yielded the plasmid pVE29 carrying the N-terminal fragment of the bt15 gene with a NcoI site at the ATG initiation codon.

According to Brizzard and Whiteley (1988), the initiation codon of the bt14 gene is a TTG codon. Similarly, a NcoI site was created at this codon for site directed mutagenesis using a 34-mer oligonucleotide with the following sequence :

20 5'-CCTATTTGAAGCCATGGTAACTCCTCCTTTTATG-3'.

In this case the sequence of the initiation codon was converted from ATATTGA to ACCATGG. This yielded the plasmid pHW44 carrying the N-terminal fragment of the bt14 gene with a NcoI site at the initiation codon.

25 In a second step, the genes were reconstructed by ligating the N-terminal gene fragments with a suitable C-terminal gene fragment yielding a bt15 and bt14 gene respectively with a NcoI site at the ATG initiation codon.

To express the bt14 and bt15 genes encoding the protoxin in E. coli, the following constructs were made:
30 pOH50 contains the bt15 gene under control of the lac promoter, pHW67 contains the bt14 gene under control of the tac promoter. Induction of a culture of the strain WK6 carrying the respective plasmids with IPTG yielded an overproduced protein.

As mentioned, the active toxic fragment of the bt15 and bt14 protoxin comprise a 63 and 60 kDa trypsin digest product respectively. Instead of expressing the whole gene, it is also possible to express a toxin encoding gene fragment or derivatives therefrom in plants. To this end, truncated bt14 and bt15 gene fragments were constructed. In order to be able to select transgenic plants producing the ICP gene products, hybrid genes of the truncated gene fragments were also made with the neo gene encoding a selectable marker as described in EP patent publication EP 0193259.

By comparison of the nucleotide sequence of the bt4, bt14 and bt15 genes respectively with the bt2 and bt18 genes respectively, the BclI site could be identified as a suitable site localized downstream of the coding sequence encoding the toxin gene fragment. To construct a truncated gene fragment and a hybrid gene of the latter with the neo gene, the filled BclI site was ligated to the filled EcoRI site of pLKM91 (Höfte et al., 1986) and the filled HindIII site of pLK94 respectively (Botterman and Zabeau, 1987). pLKM91 carries a 5' truncated neo gene fragment which codes for an enzymatically active C-terminal gene fragment of neo, and pLK94 contains translation stop codons in three reading frames. This yielded the following plasmids:
45 pHW71 carries a bt14 truncated neo-hybrid gene; pHW72 a truncated bt14 gene, pVE34 a truncated-bt15-neo hybrid gene; pVE35 a truncated bt15 gene. In a similar way as described for bt14 and bt15 in this example, and for bt2 and bt18 in previous EP applications, gene cassettes can be constructed for the bt3 and bt4 genes and the genes can be expressed in E.coli.

50

EXAMPLE 3: Purification of recombinant ICPs

Purification methods for recombinant Bt2 protoxin were described by Höfte et al. (1986). The same
55 procedure can be applied for other recombinant toxins.

EXAMPLE 4: Purification of activated toxins

Solubilized protoxins of Bt2-, Bt3-, Bt4-, Bt14-, Bt15-, Bt13-, Bt21 (in Na₂CO₃ 50mM, DTT 10 mM pH = 10) are dialyzed against 0.5 % (NH₄)₂CO₃ at pH 8 and treated with trypsin (trypsin protoxin 1 20 w/w) for 2h at 37 ° C. The activated toxin is chromatographically purified (Mono-Q column on FPLC) as described by Hofmann et al.(1988b).

5

EXAMPLE 5: Determination of the insecticidal spectrum

Recombinant protoxins or activated toxins can be evaluated for their insecticidal activity. The protoxin is dissolved in alkaline buffer containing a reducing agent (Na₂CO₃ 50 mM, DTT 10 mM pH = 10), or the toxin is used as soluble protein directly from FPLC. Protein concentrations are determined. Subsequently dilutions of the protoxin or toxin solution are prepared in PBS buffer pH = 7.4 containing 0.15 M NaCl and 0.1 % Bovine serum albumin.

Artificial medium for insect culture (e.g. the medium described by Bell and Joachim, 1976 for Manduca sexta) is poured in appropriate recipients and allowed to solidify. Subsequently a quantity of the (pro)toxin dilutions is applied on this medium and the water is allowed to evaporate under a laminar flow. This results in medium with a certain quantity of toxin coated on the surface of the artificial medium. (quantities are usually in the range of 0.1 to 10000 ng.cm²). E.g. for Bt2-toxin typical dilutions for a toxicity test on Manduca sexta are 1,5,25,125 and 625 ng.cm². First instar larvae of Manduca sexta are then applied on the medium and growth and mortality are assessed after 6 days. Mortality increases with dosage. Dose response data can be analysed in probit analysis (Finney, 1962) and the data are best summarized by an LD50 value, this is the amount of toxin which kills 50 % of the insects. The LD50 for Bt2-toxin against Manduca sexta is around 20 ng.cm².

Similar assays are possible for other insect species using a suitable diet, or similar setups are also possible applying the toxin on leaves for insects for which no artificial diet is used.

EXAMPLE 6: Binding studies

30

Toxins

All protoxins and their toxic fragments were purified according to the methods described for the Bt2- protoxin and toxin in Höfte et al. (1986) and EP patent publication EP 0193259. The activated and purified toxins are further referred to as the Bt2-, Bt3-, Bt4-, Bt14-, Bt15-, Bt13-, Bt21- and Bt22-toxins.

It has been shown that B. thuringiensis var. kurstaki HD73 produces one protein of 133 kDa encoded by a 6.6 kb type gene. A culture of this strain was grown as described by Mahillon and Delcour (1984). The autolysed culture was spun down (20 minutes at 4500 rpm in a HB4 rotor) and washed with a buffer containing 20 mM Tris, 100 mM NaCl and 0.05 % Triton X-100, pH 8. The final pellet was resuspended in this buffer (4 ml buffer for 100 ml culture). This solution was then layered onto a linear Urografin gradient (60-70%) which was centrifuged in a SW 28 rotor for 90 minutes at 18000 rpm. Crystals were collected and stored at -20 ° C until further use. Activation was performed according to Höfte et al. (1986). The purified toxin is further referred to as the Bt73-toxin.

45

Iodination of ICPs

Iodination of Bt2-, Bt3-, and Bt73-toxin was performed using the Chloramin-T method (Hunter and Greenwood, 1962). 1 mCi ¹²⁵I-Nal and 20 to 37.5 ug Chloramin-T in NaCl.P_i were added to 50 ug of purified toxin. After gentle shaking for 60 seconds. the reaction was stopped by adding 53 ug of potassium metabisulfite in H₂O. The whole mixture was loaded on a PD 10 Sephadex G-25M gelfiltration column to remove free iodine. A subsequent run on a Biogel P-60 column was carried out in order to increase the purity. Alternatively, toxins were labeled using the Iodogen method. Iodogen (Pierce) was dissolved in chloroform at 0.1 mg.ml. 100 ul of this solution was pipetted into a disposable glass vessel and dried under a stream of nitrogen gas. The vessel was rinsed with Tris buffer (20 mM Tris, pH 8.65 with 0.15 M NaCl). 50 ug of toxin (in Tris buffer) was incubated with 1 mCi of ¹²⁵I-Nal in the tube for 10 minutes. The reaction was then stopped by the addition of 1 M NaI (one fourth of the sample volume). The sample was immediately loaded onto a PD10 Sephadex G-25M column and later on a Biogel P-60 column to remove

free iodine and possible degradation products. Other toxins were iodinated using one of the above mentioned procedures.

5 Determination of specific activity of iodinated toxin

Specific activity of iodinated Bt2-, Bt3-, and Bt73-toxin samples was determined using a 'sandwich' ELISA technique according to Voller, Bidwell and Barlett (1976) in Manual of Clinical Immunology (Rose and Friedman, eds) pp. 506-512, American Society of Microbiology, Washington). Primary antibody was a
 10 polyclonal antiserum raised against Bt2-toxin and the secondary antibody was a monoclonal antibody 4D6 (unpublished results).

The conjugate used was alkaline phosphatase coupled to anti mouse IgG. The reaction intensity of a standard dilution series of unlabeled toxin and dilutions of the iodinated toxin sample (in NaCl/P_i - 0.1 % BSA) was measured. Linear regression calculations yielded the protein content of the radioactive toxin
 15 sample. The samples with the highest specific activities were used in the binding assays. Specific activities were 59400, 33000 and 19800 Ci/mole (on reference date) for Bt73-toxin (labeled according to lodogen procedure), Bt2-toxin (Chloramin-T method) and Bt3-toxin (Iodogen method) respectively.

Specific activities of other toxins were determined using a similar approach. Specific monoclonal and polyclonal antibodies for each of these toxins were raised and applied in ELISA.

20

Preparation of brush border membrane vesicles

Brush border membrane vesicles ("BBMV") from Manduca sexta, Heliothis virescens, Spodoptera littoralis, Plodia interpunctella, Mamestra brassicae, Pieris brassicae, Leptinotarsa decemlineata were
 25 prepared according to the method of Wolfersberger et al. (1987). This is a differential centrifugation method that makes use of the higher density of negative electrostatic charges on luminal than on basolateral membranes to separate these fractions.

30

Binding assay

Duplicate samples of ¹²⁵I-labeled toxin, either alone or in combination with varying amounts of unlabeled toxin, were incubated at the appropriate temperature with brush border membrane vesicles in a
 35 total volume of 100 μ l of Tris buffer (Tris 10 mM, 150 mM NaCl, pH 7.4). All buffers contained 0.1 % bovine serum albumin (BSA). The incubation temperature was 20 C. Ultrafiltration through Whatman GF/F glass fiber filters was used to separate bound from free toxin. Each filter was rapidly washed with 5 ml of ice-cold buffer (NaCl/P_i - 0.1 % BSA). The radioactivity of the filter was measured in a gammacounter (1275 Minigamma, LKB). Binding data were analyzed using the LIGAND computer program. This program
 40 calculates the bound concentration of ligand as a function of the total concentration of ligand, given the affinity (K_a or its inverse $K_d = 1/K_a$, the dissociation constant) and the total concentration of receptors or binding site concentration (R_t).

45 Determination of protein concentration

Protein concentrations of purified Bt2-, Bt3-, Bt73- and Bt15-toxin were calculated from the OD at 280 nm (measured with a Uvikon 810 P, Kontron Instruments spectrophotometer). The protein content of solutions of other toxins and of brush border membrane vesicles (BBMV) as measured according to Bradford (1976).

50

Binding of Bt2, Bt3 and Bt73 toxin to BBMV of Manduca sexta and Heliothis virescens : an example of 3 competitively binding Lepidopteran ICPs.

Bt2, Bt3 and Bt73 toxins are toxic to both Manduca sexta and Heliothis virescens: LC50 values for Manduca sexta are respectively 20.20 and 9 ng/cm² ; for Heliothis virescens the LC50's are 7.157 and 9
 55 ng/cm².

Labelled toxin, either Bt3 (0.8 nM) or Bt2 (1.05 nM) or Bt73 (1.05 nM) was incubated with BBMV in a

volume of 0.1 ml. BBMV protein concentrations were 100 ug/ml for M. sexta and for Bt2-H. virescens, for Bt3-H. virescens 150 and for Bt73-H. virescens 50 ug/ml was used. The labelled toxin was combined with varying amounts of an unlabeled toxin (competitor). After a 30 min incubation bound and free toxin were separated through filtration.

5 Figs. 1-3 show the percentages binding of respectively labelled Bt2, Bt3 and Bt73 toxin as a function of the concentration of competitor for Manduca sexta. Figs. 4-6 show these data for Heliothis virescens. The amount bound in the absence of competitor is always taken as 100 % binding. Figs. 1-6 show the binding of 125 I-labelled toxins to M. sexta (in Figs. 1, 2 and 3) and H. virescens (in Figs. 4, 5 and 6) brush border membrane vesicles ("BBMV"). Vesicles were incubated with labeled toxin [in Figs. 1 and 4: 125 I-Bt2-toxin (1.05nM); in Figs. 2 and 5: 125 I-Bt3-toxin (0.8nM); in Figs. 3 and 6: 125 I-Bt73-toxin (1.05nM) in the presence of increasing concentrations of Bt2-toxin (★), Bt3-toxin (●) or Bt73-toxin (▲). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. On M. sexta vesicles, these amounts were 1820, 601 and 2383 cpm, and on H. virescens vesicles 1775, 472 and 6608 cpm for 125 I-Bt2-, Bt3- and Bt73-toxin, respectively. Non-specific binding was not subtracted. Data were analyzed with the

15 LIGAND computer program. Each point is the mean of a duplicate sample.

Figure 1: shows the binding of 125 I Bt2 toxin to M. sexta BBMV

Figure 2: shows the binding of 125 I Bt3 toxin to M. sexta BBMV

Figure 3: shows the binding of 125 I Bt73 toxin to M. sexta BBMV

Figure 4: shows the binding of 125 I Bt2 toxin to H. virescens BBMV

20 Figure 5: shows the binding of 125 I Bt3 toxin to H. virescens BBMV

Figure 6: shows the binding of 125 I Bt73 toxin to H. virescens BBMV

The conclusions from these figures are that Bt2 and Bt3, Bt3 and Bt73, and Bt2 and Bt73 are competitively-binding ICP's both for Manduca sexta and for Heliothis virescens. Indeed Bt3 competes for the entire population of receptor sites of Bt2 in Manduca sexta (Fig.1): the % labelled Bt2 bound in the presence of 100 nM Bt3 is equal to the % Bt2 bound with 100 nM of Bt2 itself. The opposite is not true: in the presence of 100 nM Bt2 the % of labelled Bt3 is not reduced to the same level as with 100 nM of Bt3 (fig.2).

A similar reasoning is followed to observe competitiveness of other toxin combinations : Bt3 competes for the entire population of receptor sites of Bt73 (fig 3) in M. sexta, the opposite is not true (fig 2), Bt2 and Bt73 compete for the entire population of each other's binding sites (Figs. 1 and 3).

30 In Heliothis virescens : Bt2 competes for the entire population of receptor sites of Bt3 (fig 5), Bt73 competes for the entire population of receptor sites of Bt3 (fig 5) and Bt73 competes for the entire population of receptor sites of Bt2 (Fig. 4), the opposite statements are not true (Figs. 4,5 and 6).

The same data can be used in mathematical analysis (e.g. Scatchard analysis according to Scatchard, 1949 ; analysis with the LIGAND computer program according to Munson and Rodbard, 1980) to calculate the dissociation constant (Kd) of the toxin-receptor complex and the concentration of binding sites (Rt) : the results of these calculations using the LIGAND computer program were the following:

40	Bt2-M. sexta:	Kd=0.4 nM	Rt=3.4 pmol/mg vesicle protein
	Bt3-M. sexta:	Kd=1.5 nM	Rt=9.8 pmol/mg vesicle protein
	Bt73-M. sexta:	Kd=0.6 nM	Rt=4.0 pmol/mg vesicle protein
45	Bt2-H. virescens:	Kd=0.6 nM	Rt=9.7 pmol/mg vesicle protein
	Bt3-H. virescens:	Kd=1.2 nM	Rt=3.7 pmol/mg vesicle protein
50			Rt=19.5 pmol/mg vesicle protein
	Bt73-H. virescens:	Kd=0.8 nM	Rt=19.5 pmol/mg vesicle protein

55

These data demonstrate the high affinity receptor binding of the toxin (Kd's in the range of 10^{-10} to 10^{-9} M).

Binding of Bt2 and Bt14 to BBMV of *P. brassicae* : an example two non-competitively binding Lepidopteran ICPs

Bt2 and Bt14 toxins are both toxic to *P. brassicae*. LC50 values were 1.3 and 2.0 ug/ml respectively (5 ul toxin samples were applied on leaf discs fed to first instar *P. brassicae* larvae). Labelled Bt2 (1.05 nM) or Bt14 (1.4 nM) were incubated with BBMV from *P. brassicae* (100 ug protein/ml) in a volume of 0.1 ml in combination with varying amounts of unlabelled Bt2 or Bt14. After a 30 min incubation period at 22 °C the bound and free toxin were separated.

Figures 7 and 8 show the binding of ¹²⁵I-labeled toxins to *P. brassicae* brush border membrane vesicles. Vesicles were incubated with labeled toxin [in Fig. 7: ¹²⁵I-Bt2-toxin (1.05nM); in Fig. 8: ¹²⁵I-Bt14-toxin (1.4nM)] in the presence of increasing concentrate of Bt2 toxin (○) or Bt14 toxin (●). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. Non-specific binding was not subtracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample. Figure 7 shows the binding of labelled Bt2 *P. brassicae* BBMV, and Figure 8 shows the binding of labelled Bt14 *P. brassicae* BBMV.

The competition data demonstrate the presence of high affinity binding sites both for Bt2 and Bt14, as well as the almost complete absence of competition of Bt14 for the Bt2 binding sites and of Bt14 for the Bt2 binding sites. This demonstrates that Bt2 and Bt14 are non-competitively binding toxins. Hence they are useful to prevent the development of *Pieris brassicae* resistance against *B. thuringiensis* ICP's expressed in

Brassica

sp. Calculated Kd and Rt values were from these experiments were:

Bt2:	Kd = 2.8 nM, Rt = 12.9 pmol/mg vesicle protein
Bt14:	Kd = 8.4 nM, Rt = 21.4 pmol/mg vesicle protein

Binding of Bt2 and Bt15 to BBMV of *M.sexta*, *M.brassicae*, *S.littoralis* and *P.interpunctella* : an example of two non-competitively binding Lepidopteran ICPs

Bt2 and Bt15 toxins are both toxic to *M.sexta* (LC50's of 20 and 111 ng/cm² respectively). They also show activity against *M. brassicae*, *S. littoralis* and *P. interpunctella*.

Labelled Bt2 (1.05 nM) or Bt15 (0.7 nM) were incubated with BBMV from *M.sexta* (100 ug protein/ ml) in a volume of 0.1 ml in combination with varying amounts of unlabelled Bt2 or Bt15. After a 30 min incubation period at 22 °C the bound and free toxin were separated.

Figs. 9-10 show the binding of ¹²⁵I-labeled toxins to *M. sexta* brush border membrane vesicles. Vesicles were incubated with labeled toxin [in Fig. 9: ¹²⁵I-Bt2-toxin (1.05nM); in Fig. 10: ¹²⁵I-Bt15-toxin (0.7nM)] in the presence of increasing concentrations of Bt2-toxin (○) or Bt15-toxin (●). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. Non-specific binding was not subtracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample. Figure 9 shows the data for binding of labelled Bt2, and Figure 10 shows the binding of labelled Bt15.

The competition data demonstrate the presence of high affinity binding sites both for Bt2 and Bt15, as well as the complete absence of competition of Bt15 for the Bt2 binding sites and of Bt2 for the Bt15 binding sites. This demonstrates that Bt2 and Bt15 are non-competitively binding toxins. Hence the combination of Bt2 and Bt15 is useful to prevent the development of resistance of *M.sexta* against *B. thuringiensis* ICP's expressed in tobacco or other crops in which *Manduca* sp. are a pest. Calculated Kd and Rt values are:

Bt2:	Kd = 0.4 nM, Rt = 3.4 pmol/mg vesicle protein
Bt15:	Kd = 0.3 nM Kd2 = 2.9 nM, Rt1 = 5.9 and Rt2 = 6.7 pmol/mg vesicle protein (2 distinct high affinity receptor sites are present).

Similar studies were performed for *M. brassicae*, *S. littoralis* and *P. Interpunctella*. Although LD50, Kd and Rt values differed substantially the essential observation that Bt2 and Bt15 are both toxic and are non-

competitively binding toxins was confirmed in these three insect species. Thus it is also a useful toxin combination to prevent resistance of M. brassicae against ICP's in Brassica sp. or to prevent resistance of Spodoptera species against ICP's expressed in any of the crop plants in which Spodoptera species are a pest.

5

Binding of Bt2 and Bt4 to BBMV of M. sexta: an example of two non-competitively binding Lepidopteran ICPs

- 10 Both Bt2 and Bt4 toxins are toxic to Manduca sexta. LD50 values are 20 and 10 ng.cm² respectively. No mutual competition of Bt2 for binding of labelled Bt4 and of Bt4 for binding of labelled Bt2 was observed, demonstrating that Bt2 and Bt4 are non-competitively binding toxins.

15 Binding of Bt15 and Bt18 to BBMV of S. littoralis: an example of two non-competitively binding Lepidopteran ICPs

- Both Bt15 and Bt18 toxins are toxic to S. littoralis. LD 50 values are 93 and 88 ng toxin:cm² respectively. Labelled Bt15 (0.7 nM) or Bt18 (0.9 nM) were incubated with 100 ug of vesicle protein from S. littoralis in combination with varying amounts of unlabelled Bt15 or Bt18 toxin. After a 45 min incubation period bound and free toxin were separated. Binding data demonstrate high affinity binding for both Bt15 and Bt18 to S. littoralis BBMV. As illustrated in figures 11 and 12, the entire population of receptor sites of Bt15 was not saturable with Bt18, neither was the entire population of receptor sites of Bt18 saturable with Bt15.

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Binding of Bt13 and Bt22 to BBMV of L. decemlineata : an example of two non-competitively binding Coleopteran ICPs.

- 30 Both Bt13 and Bt22 toxins are toxic to L. decemlineata. LD 50 values are 0.8 and 1.1 ug toxin/ml respectively. Labelled Bt13 (1 nM) or Bt22 (0.7 nM) were incubated with 100 ug of vesicle protein:ml from S. littoralis in combination with varying amounts of unlabelled Bt13 or Bt22 toxin. After a 45 min incubation period bound and free toxin were separated. Binding data demonstrate high affinity binding for both Bt13 and Bt22 to S. littoralis BBMV. The entire population of receptor sites of Bt13 was not saturable with Bt22. 35 neither was the entire population of receptor sites of Bt22 saturable with Bt13.

Binding of Bt2 and Bt18 to BBMV of M. sexta: an example of two non-competitively binding Lepidopteran ICPs.

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- Both Bt2 and Bt18 toxins are toxic to M. sexta, and LD 50 values are 20 to 73 ng toxin cm² respectively. Labelled Bt2 (1.05nM) or Bt18 (0.7nm) were incubated with 100 ug.ml of vesicle protein from M. sexta in combination with varying amounts of unlabelled Bt2 or Bt18 toxin. After a 45 min. incubation period, bound and free toxin were separated. Binding data (Figs. 11-12) demonstrate high affinity binding for both Bt2 and Bt18 to M. sexta BBMV. The entire population of receptor sites of Bt2 was not saturable with Bt18, neither 45 was the entire population of receptor sites of Bt18 saturable with Bt2. Calculated Kd and Rt values are:

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Bt2:	Kd = 0.4 nM, Rt = 3.4 pmol:mg vesicle protein.
Bt18:	Kd1 = 0.04 nM, Rt1 = 2.2 pmoles/mg vesicle protein and Kd2 = 168nM Rt2 = 194 pmoles/mg vesicle protein (2 distinct receptor sites for Bt18 are present).

- 55 A list of non-competitively binding anti-Lepidopteran ICP combinations and anti-Coleopteran ICP combinations is given below, together with their common target insect species in which non-competitiveness has been demonstrated

Bt2-Bt15 (Manduca sexta, Spodoptera littoralis, Pieris brassicae, Mamestra brassicae, Plodia interpunctella)
 Bt2-Bt18 (Manduca sexta, Spodoptera littoralis)

- Bt2-Bt14 (Pieris brassicae)
 Bt2-Bt4 (Manduca sexta)
 Bt15-Bt18 (Manduca sexta, Spodoptera littoralis)
 Bt14-Bt15 (Pieris brassicae)
 5 Bt15-Bt4 (Manduca sexta)
 Bt18-Bt4 (Manduca sexta)
 Bt18-Bt14 (Pieris brassicae)
 Bt18-Bt4 (Manduca sexta)
 Bt13-Bt21 (Leptinotarsa decemlineata)
 10 Bt13-Bt22 (Leptinotarsa decemlineata)
 Bt21-Bt22 (Leptinotarsa decemlineata)

This list is not believed to be exhaustive, and it will be clear that the competitiveness of novel toxin combinations, even of toxins which are still to be discovered, can be investigated using a similar approach for any given insect species.

- 15 The above list of toxin combinations for a given insect pests will immediately suggest to those skilled in the art a number of host plants in which the expression of these combinations is useful : e.g. the combination of Bt2-Bt14 in Brassica to prevent resistance of Pieris brassicae against the ICP's expressed in the plant.

20 EXAMPLE 7: Selection for resistance of Manduca sexta (tobacco hornworm)

- A selection experiment consists in exposing a large number of larvae to a concentration of toxin in diet killing e.g. 50-90 % of the larvae. The surviving larvae are again exposed to toxin concentrations killing a similar proportion of the larvae and this process is continued for several generations. The sensitivity of the larvae to the toxin is investigated after each four generations of selection.

We performed selections for 20 generations with Bt2 alone, with Bt18 alone and with a 1/4 by weight Bt2/Bt18 mixture.

- LC50 values of our reference strain for Bt2, Bt18 and the 1/4 Bt2.Bt18 mixture respectively were the following : 20 ng/cm², 73 ng/cm² and 62 ng/cm² of diet.

- 30 Selection was initiated at with concentrations killing around 75 % of the animals. After 4 generations of selection survival increased in both the Bt2 and the Bt18 selection to around 70 %, no such increase was obtained in the selection with the combination of Bt2/Bt18. Dosages were again increased to calculated LC75 values. This was repeated every 4 generations. The selection process was thus continued to the 20th generation.

Final results were the following (LC50 of the 20th generation)

40	- Bt2 selection:	LC50 Bt2 6400 ug/g (320 times decreased sensitivity)
	- Bt18 selection:	LC50 Bt15 15100 ug/g (207 times decreased sensitivity)
	- Bt2/Bt18 selection:	LC50 Bt2/Bt15 181 ug/g (3 times decreased sensitivity).

Thus the decrease in sensitivity was about 100 times slower in the combined selection experiment.

- 45 Receptor binding in the three selected strains was investigated with Bt2 and Bt18 and compared to those of the reference strain (non-selected strain).

Binding characteristics reference strain :

50	Bt2:	Kd = 0.4 nM, Rt=3.4 pmol/mg vesicle protein
	Bt18:	Kd1=0.04 nM, Rt1=2.2 pmoles/mg vesicle protein and Kd2=168nM, Rt2=194 pmoles/mg vesicle protein (2 distinct receptor sites for Bt18 are present).

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Figures 11 and 12 show the binding of ¹²⁵I-labeled toxins to M. sexta brush border membrane vesicle. Vesicles were incubated with labeled toxin [in Fig. 11: ¹²⁵I-Bt2-toxin (1.05nM); in Fig. 12: ¹²⁵I-Bt18-toxin (0.7nm)] in the presence of increasing concentrations of Bt2-toxin (○), or Bt18-toxin (●). Binding is

expressed as percentage of the amount bound upon incubation with labeled toxin alone. Non-specific binding was not subtracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample.

The Bt2 selected strain showed no detectable high affinity binding of Bt2 whereas its Bt18 binding characteristics remained close to the reference strain. (Bt18: $K_d1 = 0.03$ nM, $Rt1 = 2.8$ pmoles/mg vesicle protein and $K_d2 = 199$ nM, $Rt2 = 109$ pmoles/mg vesicle protein - 2 distinct receptor sites for Bt18 are still present).

The Bt18 selected strain lost the high affinity receptor site for Bt18. The lower affinity site for Bt18 was still present in lower concentration than in the reference strain ($K_d = 189$ nM, $Rt = 43$ nM). Bt2 binding site concentration increased markedly compared to the reference strain ($K_d = 0.4$ nM, $Rt = 20.8$ pmoles/mg vesicle protein. This strain had a Bt2 sensitivity of $LC_{50} = 4$ ng/cm². Thus, its sensitivity for Bt2 had increased as compared to the reference strain ($LC_{50} = 20$ ng/cm²).

The Bt2/Bt18 selected strain showed a slight but statistically non-significant decrease in Bt18 binding site concentration. (Bt2: $K_d = 0.4$ nM, $Rt = 3.4$ pmol/mg vesicle protein ; Bt18 : $K_d1 = 0.04$ nM, $Rt1 = 1.0$ pmoles/mg vesicle protein and $K_d2 = 168$ nM, $Rt2 = 194$ pmoles/mg vesicle protein (2 distinct receptor sites for Bt18 are present) .

These data demonstrate that in the two selection lines where resistance occurred, the mechanism was situated at the receptor level. Changes in receptor site are shown to be the most likely mechanism of resistance to B. thuringiensis ICPs.

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EXAMPLE 8: Separate transfer of two ICP genes comprised within individual transcriptional units to the genome of plant cells

Two procedures are described for the combined expression of bt2 and bt15 in transgenic tomato plants. These procedures are based on the transfer of two chimeric ICP genes not linked within the same DNA fragment to the genome of the plant of interest.

A first procedure is based on sequential transformation steps in which a plant already transformed with a first chimeric ICP gene is retransformed in order to introduce a second ICP gene. The sequential transformation makes use of two different selectable marker genes, being the resistance genes for kanamycin and phosphinotricin acetyl transferase (PPT) which confers resistance to phosphinotricin (use of both selectable markers is already described in De Block et al., 1987). The second procedure is based on the cotransformation of two chimeric ICP genes localized on different plasmids in a single step. The integration of both ICP genes can be selected by making use of the two selectable markers conferring resistance to Km and PPT linked with the respective ICP genes. In this example, we describe Ti-plasmid vectors for Agrobacterium mediated transformation of these chimeric ICP genes.

In EP publication 0193259, pGSH163 has been described. This plasmid contains the following chimeric genes between the T-DNA border repeats : a gene fragment encoding the toxin part of bt2 gene under control of the TR2' promoter and the neo gene under control of the TR1' promoter. The 3' ends of the T-DNA gene 7 and octopine synthase respectively provide information for the 3' end formation of transcripts.

A chimeric bt15 gene containing a gene fragment encoding the toxin part of bt15 under the control of the TR2' promoter was constructed in the following way. pOH50 consists of pUC18 with the whole bt15 gene under control of the lac promoter. A HindIII-BglII fragment was cloned in pMa5-8 yielding pJB3. By site directed mutagenesis as described, a NcoI site was created at the initiation codon to yield pVE29. A fragment containing the truncated gene fragment of the bt15 gene with a translational stop codon was obtained by isolation of BclI-ClaI from pOH50 and cloning in pLK91 yielding pHW38. The whole toxin gene fragment was reconstructed under control of the tac promoter yielding pVE35 by ligation of a ClaI-PstI fragment from pHW38, a NcoI-ClaI fragment from pVE29 and a NcoI-PstI fragment from pOH48. A truncated bt15 gene fragment with a NcoI site at the initiation codon was obtained from pVE35 as a 1980 NcoI-BamHI fragment and cloned in pGSJ141. digested with ClaI and BamHI. pGSJ141 has been described in EP application n° 88402115.5. Ligation of the filled ClaI site to the filled NcoI site yielded a chimeric TR2'-bt15 truncated - 3'g7 construct (pTVE47). As a selectable marker in this plasmid, the bar gene encoding phosphinothricin acetyl transferase and conferring resistance to PPT was used. A chimeric bar gene containing the bar gene under control of the 35S promoter and followed by the 3' end of the octopine synthase was introduced in pTVE47. From pDE110, a 35S-bar-3'ocs fragment was obtained as a StuI-HindIII fragment and was cloned in pTVE47 digested with PstI and HindIII. This yielded the plasmid pTHW88 which contains the truncated bt15 gene under control of the TR2' promoter and the bar gene under control of the 35S promoter comprised between the T-DNA border repeats. Plasmid pGSH163 is

cointegration type Ti-plasmid vector, whereas pTHW88 is a binary type Ti-plasmid vector as described in EP publication 0193259.

Both plasmids were mobilized in the *A. tumefaciens* strain C58C1Rif (pGV2260) according to Deblaere et al., (1988). In the sequential transformation procedure, tomato has been transformed according to De Block et al., 1987 with the *A. tumefaciens* strain C58C1Rif carrying pGS1163 resulting from the cointegration of pGSH163 and pGV2260. Individual transformants were selected for kanamycin resistance, and regenerated plants were characterized for expression of the truncated *bt2* gene according to Vaeck et al., (1987). One representative transformant was subsequently retransformed with the *A. tumefaciens* strain C58C1Rif (pGV2260) (pTHW88), and transformants were selected for PPT resistance. Using the cotransformation procedure, the respective *Agrobacteria* strains carrying the cointegrate vector pGS1163 and the binary vector pTHW88 were used for transformation of tomato. Individual plants were selected for resistance to Km and PPT.

Schematically shown in Fig. 15 are:

15	a)	bt15 N-terminal gene fragment with NcoI site introduced at ATG initiation codon.
	construction of pVE29:	
	b)	bt15 C-terminal truncated gene fragment under control of the tac promoter.
20	construction of pVE35:	
	c)	binary T-DNA vector with a chimeric <i>bt15</i> gene and a chimeric <i>bar</i> gene within the T-DNA border repeats.
	construction of pTHW88:	

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In both cases, co-expression of the two ICP genes in the individual transformants was evaluated by insect toxicity tests as described in EP publication 0193259 and by biochemical means. Specific RNA probes allow to quantitate the transcript levels, monoclonal antibodies cross-reacting with the respective gene products allow to quantitate the respective gene products in ELISA tests and specific DNA probes allow to characterize the genome integrations.

These procedures also could be applied when one or both ICP genes are part of a hybrid gene. For example, the same strategy as described could be followed with the plasmid vectors pGSH152, containing a chimeric truncated-neo *bt2* hybrid gene under control of the TR2' promoter and pTHW88 in suitable *Agrobacterium* strains.

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EXAMPLE 9: Transfer of two chimeric ICP genes linked within the same DNA to the genome of plant cells

The strategy used is based on the organization of two independent chimeric ICP genes between the T-DNA border repeats of a single vector. Binding studies indicated that the Bt2 and Bt14 toxins are two non-competitively binding ICPs with insecticidal activity towards *Pieris brassicae*. For expression in plants, both the *bt2* and *bt14* genes can be co-expressed to prevent insect resistance development. For the design of a plasmid vector with each ICP gene under the control of a separate promoter, several possibilities can be envisaged: 1) three chimeric constructs carrying the truncated *bt2* and *bt14* genes and a selectable marker, respectively, or 2) a hybrid of a truncated gene fragment (*bt2* or *bt14*) and the *neo* gene can be used in combination with a truncated *bt14* or *bt2* gene. This example describes the construction of the vector pTHW94 for plant transformation carrying the following chimeric ICP genes between the T-DNA border repeats: a truncated *bt2* gene fragment under the control of the TR2' promoter and a hybrid truncated *bt14-neo* gene under the control of the TR1' promoter. The 3' end of the T-DNA gene 7 and octopine synthase respectively provide information for proper 3' end formation. pTHW94 is being deposited at Deutsche Sammlung von Mikroorganismen und Zellkulturen ("DSM"), Braunschweig, Federal Republic of Germany.

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Schematically shown in Fig. 16 are:

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a) construction of pHW44:	<u>bt14</u> N-terminal gene fragment with NcoI site introduced at ATG initiation codon.
b) construction of pHW67:	reconstruction of the <u>bt14</u> gene under control of the tac promoter.
c) construction of pHW71:	construction of a hybrid <u>bt14</u> ox-neo gene under control of the tac promoter.
d) construction of pTHW94:	binary T-DNA vector with a chimeric <u>bt14</u> gene and a chimeric <u>bt2</u> gene within the T-DNA border repeats.

The pTHW94 vector is a binary vector derived from pGSC1701A2 and is mobilized into the *Agrobacterium* strain C58C1Rif (pMP90). This strain was used to transform *Brassica napus* according to the procedure described by De Block et al. (in preparation). Transformants are selected on Km, and regenerated plants are analyzed for expression of both ICP gene products by insect toxicity tests and biochemical tests.

EXAMPLE 10: Expression of two ICP genes in a hybrid construct

In order to obtain a combined and simultaneous expression of two ICP genes, truncated gene fragments encoding the toxic parts of two different ICPs can be fused in a proper reading frame and placed as a hybrid gene under the control of the same promoter in a chimaeric gene construct. Toxic cores from certain ICPs can be liberated from their protoxins by protease activation at the N- and/or C- terminal end. Thus, hybrid genes can be designed with one or more regions encoding protease cleavage site(s) at the fusion point(s) of two or more ICP genes.

The simultaneous co-expression of bt2 and bt14 genes can be obtained by constructing a hybrid gene composed of a truncated bt14 gene fragment fused to a truncated bt2 gene fragment. Schematically shown in Figure 17 is the construction of such a hybrid bt2-bt14 gene with a C-terminal bt2 gene fragment (bt860) encoding the toxic core of the Bt2 protoxin in frame with a C-terminal truncated bt14 gene fragment encoding the toxic core of the Bt14 protoxin. In practice, the BclI site in the bt2 gene localized downstream of the trypsin cleavage site can be fused in frame with the NcoI site introduced at the N-terminal end of the truncated bt14 gene fragment. To this end, the plasmids pLBKm860 (EP publication 0193259) and pHW67 are used. pLBKm860 contains a hybrid bt2-neo gene under control of the lambda P_L promoter. The bt2 gene moiety in the hybrid gene is a C-terminal truncated bt2 gene fragment, indicated as bt860 (in Fig. 17) (see also Vaeck et al. 1987). The construction of pHW67 is described in Fig. 16. pHW67 contains a C-terminal truncated bt14 gene fragment (bt14tox) with a NcoI site at the ATG initiation codon, a translation stop codon located at the BclI site of the intact bt14 gene and a BamHI site downstream of the whole gene fragment. To fuse both gene fragments in the proper reading frame, the BclI and NcoI ends of the respective plasmids are treated with Klenow DNA polymerase and S1 nuclease as indicated in Figure 16. The resulting plasmid pJB100 contains the hybrid bt860-bt14tox gene under control of the lambda P_L promoter and directs the expression in *E. coli* of a fusion protein with the expected mobility on SDS-PAGE.

Crude extracts of the *E. coli* strain show the toxicity of the fusion protein, expressed by the strain, against *P. brassicae*. It has also been confirmed by N-terminal amino acid sequence analyses of the fusion protein produced by the *E. coli* strain that the N-terminal amino acids from the Bt14 protoxin are processed upon activation. The bt2-bt14 hybrid gene product has thus two potential protease cleavage sites. Subsequently, this hybrid gene can be inserted into a vector for plant transformation and placed under control of a suitable promoter and transferred to the genome of a plant of interest (EP publication 0,193,259).

Table 1

Gene	Bt strain	Host range	amino acids encoded	predicted MW(kDa) of encoded aminoacids	Disclosure of nucleotide sequence
bt3	HD-1 kurstaki	L	1176	133.2	Schnepf et al., 1985
bt2	berliner 1715	L	1155	131	Höfte et al., 1986
bt73	HD-73	L	1178	133.3	Adang et al, 1985
bt14	HD-68 aizawai	L	1207	138	Brizzard and Whitely, 1988
bt15	entomocidus HD-110	L	1189	134.8	Fig. 14
bt4	entomocidus HD-110	L	1165	132.5	Fig. 13
bt18	darmstadiensis HD-146	L	1171	133	EP appln. 88402241.9
bt13	BtS1, DSM4288 22/10/87	C	644	73.1	EP appln. 88402115.5
bt21	BtPGSI208, DSM 5131, 19/1/89	C	651	74.2	EP appln. 89400428.2

Table 1 (continued)

Gene	Bt strain	Host range	amino acids encoded	predicted MW(kDa) of encoded aminoacids	Disclosure of nucleotide sequence
bt22	BtPGSI245, DSM 5132, 19/1/89	C	1138	129	EP appln. 8940028.2
P2	HD-263	L/D	633	70.9	Donovan et al, 1988
Cry B2	HD-1	L	633	70.8	Widner and Whiteley, 1989

REFERENCES

- Adang M., Staver M., Rocheleau T., Leighton J., Barker R. and Thompson D. (1985), Gene 36, 289-300.
- Barton K., Whiteley H. and Yang N.-S. (1987), Plant Physiol. 85, 1103-1109.
- Bernard H., Remaut E., Hersfield M., Das H., Helinski D., Yanofski C. and Franklin N. (1979), Gene 5, 59-76.
- Bell R. and Joachim F. (1976), Ann. Entomol. Soc. Am. 69, 365-373.
- Botterman J. and Zabeau M. (1987), DNA 6, 583-591.
- Bradford M. (1976), Anal. Biochem. 72, 248-254.
- Brattsten L., Holyoke C., Leeper J. and Raffa K. (1986), Science 231, 1255-1260.
- Brizzard B. and Whiteley H. (1988), Nucleic Acids Research 16, 4168-4169.
- Deblaere R., Reynaerts A., Höfte H., Hernalsteens J-P, Leemans J. and Van Montagu M. (1988), Methods in Enzymol. 153, 277-292.
- De Block M., Botterman J., Vandewiele M., Dockx J., Thoen, Gosselé V., Rao Movva, Thompson C., Van Montagu M. and Leemans J. (1987), EMBO J. 6, 2513-2518.
- De Boer H., Comstock L. and Vasser M. (1983), Proc. Natl. Acad. Sci. USA 80, 21-25.
- de Framond A., Back E., Chilton W., Kayes L. and Chilton M-D (1986), Mol. Gen. Genet. 202, 125-131.
- De La Pena and Schell (1986), Nature 325, 274-276.
- Delauney A., Tabaeizadeh Z. and Verma D. (1988), Proc. Natl. Acad. Sci. USA 85, 4300-4304.
- Depicker A., Herman L., Jacobs A., Schell J. and Van Montagu M. (1985), Mol. Gen. Genet. 201, 477-484.
- Donovan W., Dankoscik C. and Gilbert W. (1988), J. Bacteriol. 170, 4732-4738.
- Dulmage H.T and cooperators (1981), In : Microbial control of pests and plant diseases 1970-1980 (Ed. H.D. Burges), Academic Press. 193-222.
- Finney D. (1962), Probit Analysis (University Press, Cambridge), pp. 50-80.
- Fischhoff D., Bowdish K., Perlak F., Marrone P., McCormick S., Niedermeyer J., Dean D., Kuzano-Kretzmer K., Mayer E., Rochester D., Rogers S. and Fraley R. (1987), Bio/Technology 5, 807-812.
- Franck, Guilley, Jonard, Richards and Hirth (1980), Cell 21, 285-294.
- French B., Maul H. and Maul G. (1986), Anal. Biochem. 156, 417-423.
- Fuller F. (1982), Gene 19, 43-54.
- Gardner, Howarth, Hahn, Brown-Luedi, Shepard and Messing, Nucl. Acids Res. 9, 2871-2887.
- Goldberg L. and Margalit J. (1977), Mosq. News 37, 355-358.

- Goldman I., Arnold J. and Carlton B. (1986), *J. Invert. Pathol.* 47, 317-324.
- Gould F. (1988), *Bioscience* 38, 26-33.
- Haider M., Knowles B. and Ellar D. (1986), *Eur. J. Biochem.* 156, 531-540.
- Hofmann C., Lüthy P., Hütter R. and Pliska V. (1988a), *Eur. J. Biochem.* 173, 85-91.
- 5 - Hofmann C., Vanderbruggen H., Höfte H., Van Rie J., Jansens S. and Van Mellaert H. (1988b), *Proc. Natl. Acad. Sci. USA* 85, 7844-7848.
- Höfte H., Van Rie J., Jansens S., Van Houtven A., Verbruggen H. and Vaeck M. (1988), *Appl. Environ. Microbiol.* 54, 2010-2017.
- Höfte H., De Greve H., Seurinck J., Jansens S., Mahillon J., Ampe C., Vanderkerckhove J.,
- 10 Vanderbruggen H., Van Montagu M., Zabeau M. and Vaeck M. (1987), *Eur. J. Biochem.* 161, 273-280.
- Hsiung H. and Becker G. (1988), *Biotech. and Genetic Engin. Rev.* 6, 43-65.
- Hull and Howell (1987), *Virology* 86, 482-493.
- Hunter W. and Greenwood F. (1962), *Nature* 194, 495-496.
- Kozak M. (1987), *Mol. Cell. Biol.* 7, 3438-3445.
- 15 - Krebbers E., Herdies L., De Clercq A., Seurinck J., Leemans J., Van Damme J., Segura M., Gheysen G., Van Montagu M. and Vandekerckhove J. (1988), *Plant Physiol.* 87, 859-866.
- Knowles B. and Ellar D. (1986), *J. Cell. Sci.* 83, 89-101.
- Krieg A., Huger A., Langenbruch G. and Schnetter W. (1983), *Z. Ang. Ent.* 96, 500-508.
- Krieg A. and Langenbruch G. (1981), In : *Microbial control of pests and plant diseases 1970-1980*
- 20 (Ed. H.D. Burges), Academic Press, 837-886.
- Kirsch K. and Schmutterer H. (1988), *J. Appl. Ent.* 105, 249-255.
- Kronstad J., Schnepf H. and Whiteley H. (1983), *J. Bacteriol.* 154, 419-428.
- Mahillon J. and Delcour J. (1984), *J. Microbiol. Methods* 3, 69-73.
- Maxam A. and Gilbert W. (1980), *Methods in Enzymol.* 65, 499-560.
- 25 - McGaughey W. (1985), *Science* 229, 193-195.
- McGaughey W. and Beeman R. (1988), *J. Econ. Entomol.* 81, 28-33.
- Munson P. and Rodbard D. (1980), *Anal. Biochem.* 107, 220-239.
- Pazkowski and cooperators (1984), *EMBO J* 3, 2717-2722.
- Peleman J., Boerjan W., Engler G., Seurinck J., Botterman J., Alliotte T., Van Montagu M. and Inzé
- 30 D. (1989), *The Plant Cell* 1, 81-93.
- Remaut E., Stanssens P. and Fiers W. (1981), *Gene* 15, 81-93.
- Sandler S., Stayton M., Townsend J., Ralston M., Bedbrook J. and Dunsmuir P. (1988), *Plant Mol. Biol.* 11, 301-310.
- Scatchard G. (1949), *Ann. N.Y. Acad. Sci.* 51, 660-672.
- 35 - Schocher R., Shillito R., Saul M., Pazkowski J. and Potrykus I. (1986) *Bio-technology* 4, 1093-1096.
- Shields (1987), *Nature* 328, 12-13.
- Schnepf H., Wong H. and Whiteley H. (1985), *J. Biol. Chem.* 260, 6264-6272.
- Stanssens P., Remaut E. and Fiers W. (1985), *Gene* 36, 211-223.
- Stanssens P., McKeown Y., Friedrich K. and Fritz H. (1987) : "Oligo-nucleotide directed construction
- 40 of mutations by the gapped duplex DNA method using the pMa/c plasmid vectors", published in the Collection of Experimental Procedures distributed at the EMBO course entitled "Directed mutagenesis and protein engineering" in July 1987 at the Max Planck Institut für Biochemie, Martinsried, FRG.
- Stone T., Sims S. and Marrone P. (1989), *J. Invert. Pathol.* 53, 228-234.
- Vaeck M., Reynaerts A., Höfte H., Jansens S., De Beukeleer M., Dean C. Zabeau M., Van Montagu
- 45 M. and Leemans J. (1987), *Nature* 327, 33-37.
- Voller, Bidwell and Barlett (1976), In : *Manual of Clinical Immunology* (Eds. Rose and Friedman), pp. 506-512, American Society of Microbiology, Washington
- Velten J., Velten L., Hain R. and Schell J. (1984), *EMBO J.* 3, 2723-2730.
- Velten J. and Schell J. (1985), *Nucl. Acids Res.* 13, 6981-6998.
- 50 - Widner W. and Whiteley H. (1989), *J. Bacteriol.* 171, 965-974.
- Wolfersberger M., Lüthy P., Maurer A., Parenti P., Sacchi V., Giordana B. and Hanozet G. (1987), *Comp. Biochem. Physiol.* 86, 301-308.
- Yanisch-Perron C., Vieira J. and Messing J. (1985), *Gene* 33, 103-119.

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Claims

1. A cell of a plant, characterized by: at least two B. thuringiensis genes stably inserted into the genome

of said plant; each of said genes encoding a different non-competitively binding insecticidal crystal protein for an insect species; whereby at least two different insecticidal crystal proteins can be produced by said cell which do not bind competitively to the brush border membrane of the columnar midgut epithelial cell of said insect species.

5 2. The cell of claim 1 wherein at least one marker gene, encoding a protein or polypeptide which renders said cell easily distinguishable from cells which do not contain said protein or polypeptide, is in the same genetic locus as at least one of said genes.

3. The cell of claim 1 or 2, wherein each of said genes is under the control of a separate promoter capable of directing gene expression in said cell and is provided with a separate signal for 3' end formation and within a same transcriptional unit.

10 4. The cell of claim 2 or 3, in which said marker DNA is under the control of a separate promoter capable of directing gene expression in said plant cell and is provided with a signal for 3' end formation within a transcriptional unit.

5. The cell of claim 1 or 2, wherein said genes are within a same transcriptional unit and under the control of a single promoter.

6. The cell of claim 5, wherein said marker gene is fused with at least one of said genes and is within said same transcriptional unit and under the control of said promoter.

7. The cell of claim 5 or 6, wherein a DNA fragment, encoding a protease sensitive amino acid sequence, is in said same transcriptional unit as said genes and intercalated in frame between said genes.

20 8. The cell of claim 5 or 6, wherein an intergenic DNA sequence allowing reinitiation of translation, is in said same transcriptional unit as said genes and intercalated between said genes.

9. The cell of anyone of claims 1 to 8, wherein two or three of said genes encode insecticidal proteins having activity against Lepidoptera species, particularly the following genes: bt2 and/or bt3 and/or bt73 and/or bt4 and/or bt14 and/or bt15 and/or bt18.

25 10. The cell of any of claims 1 to 8, wherein said genes encode insecticidal proteins having activity against a Coleoptera species, particularly the following genes: bt13, and/or bt21 and/or bt22.

11. The cell of any of claims 2 to 10 wherein said marker DNA is an herbicide resistance gene, particularly a sfr or sfrv gene, a gene encoding a modified target enzyme for a herbicide having lower affinity for the herbicide, particularly a modified 5-EPSP as target for glyphosate or a modified glutamine synthetase as target for a GS inhibitor, an antibiotic resistance gene, particularly NPTII.

30 12. The cell of any of claims 3 to 6, wherein said promoter is a constitutive promoter, particularly a 35S promoter, or a 35S3 promoter, a PNOS promoter, a POCs promoter, a wound inducible promoter, particularly a TR1' or TR2' promoter, a promoter which directs gene expression selectively in plant tissue having photosynthetic activity, particularly a SSU promoter, a tissue-specific promoter, particularly a tuber-specific promoter, or a stem-specific promoter or a seed-specific promoter.

13. A vector suitable for transforming a cell of a plant, particularly a plant capable of being infected with Agrobacterium, comprising said genes of any of claims 1 to 12.

40 14. A process for producing a plant having improved insect resistance and having said genes of any of claims 1 to 12 stably integrated into the nuclear genome of their cells, characterized by the non-biological steps of transforming a cell of said plant by introducing said genes into the nuclear genome of said cell and regenerating said plant and reproduction material from said cell.

15. A plant cell culture, containing the plant cell of any claims 1 to 12.

16. A plant, containing the plant cell of any of claims 1 to 12.

45 17. A plant, particularly brassica, tomato, tobacco, cotton or lettuce, containing the plant cell of any of claims 1 to 12, wherein said genes are particularly bt2 and bt15.

18. A plant, particularly brassica, tomato, tobacco or cotton or lettuce, containing the plant cell of any of claims 1 to 12, wherein said bt genes are particularly bt73 and bt15.

19. A plant, particularly tomato, tobacco, cotton, containing the plant cell of any of claims 1 to 12, wherein said genes are particularly bt2 and bt18.

50 20. A plant, particularly brassica, containing the plant cell of any of claims 1 to 12, wherein said genes are particularly bt2 and bt14.

21. A plant, particularly tomato or tobacco, containing the plant cell of any of claims 1 to 12, wherein said genes are particularly bt2 and bt4.

22. A plant, particularly tomato, cotton, containing the plant cell of any of claims 1 to 12, wherein said genes are particularly bt15 and bt18.

23. A plant, particularly brassica, containing the plant cell of any of claims 1 to 12, wherein said genes are particularly bt14 and bt15.

24. A plant, particularly potato, containing the plant cell of any of claims 1 to 12, wherein said genes are

particularly bt13 and bt21.

25. A plant, particularly potato, containing the plant cell of any of claims 1 to 12, wherein said genes are particularly bt21 and bt22.

26. A plant, particularly potato, containing the plant cell of any of claims 1 to 12, wherein said genes are particularly bt13 and bt22.

27. The cell of anyone of claims 1-12, made by a process as described hereinabove.

28. The plant of anyone of claims 15-26, made by a process as described hereinabove.

29. A method for rendering a plant resistant to an insect species by transforming the plant with said genes of any of claims 1-12.

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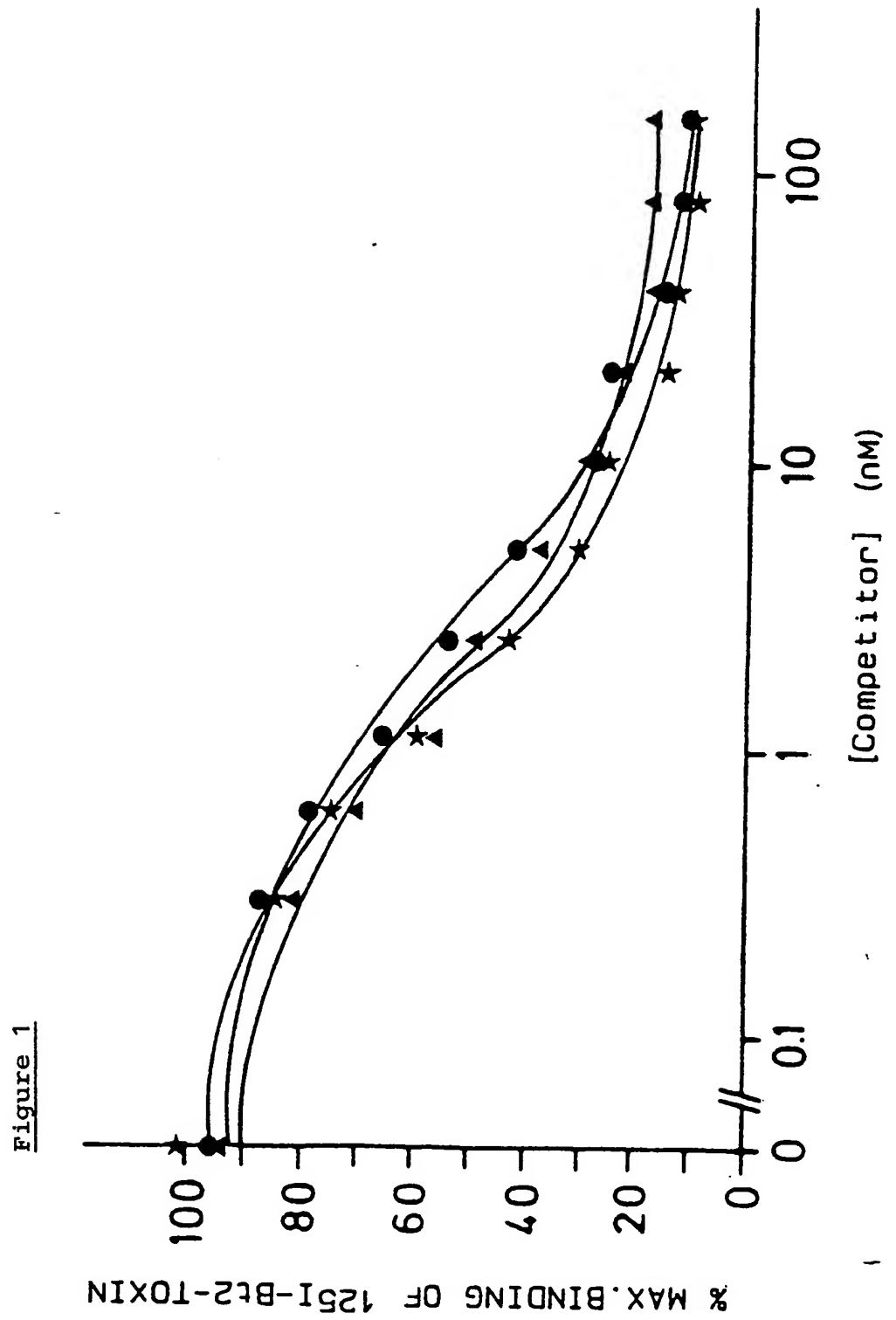


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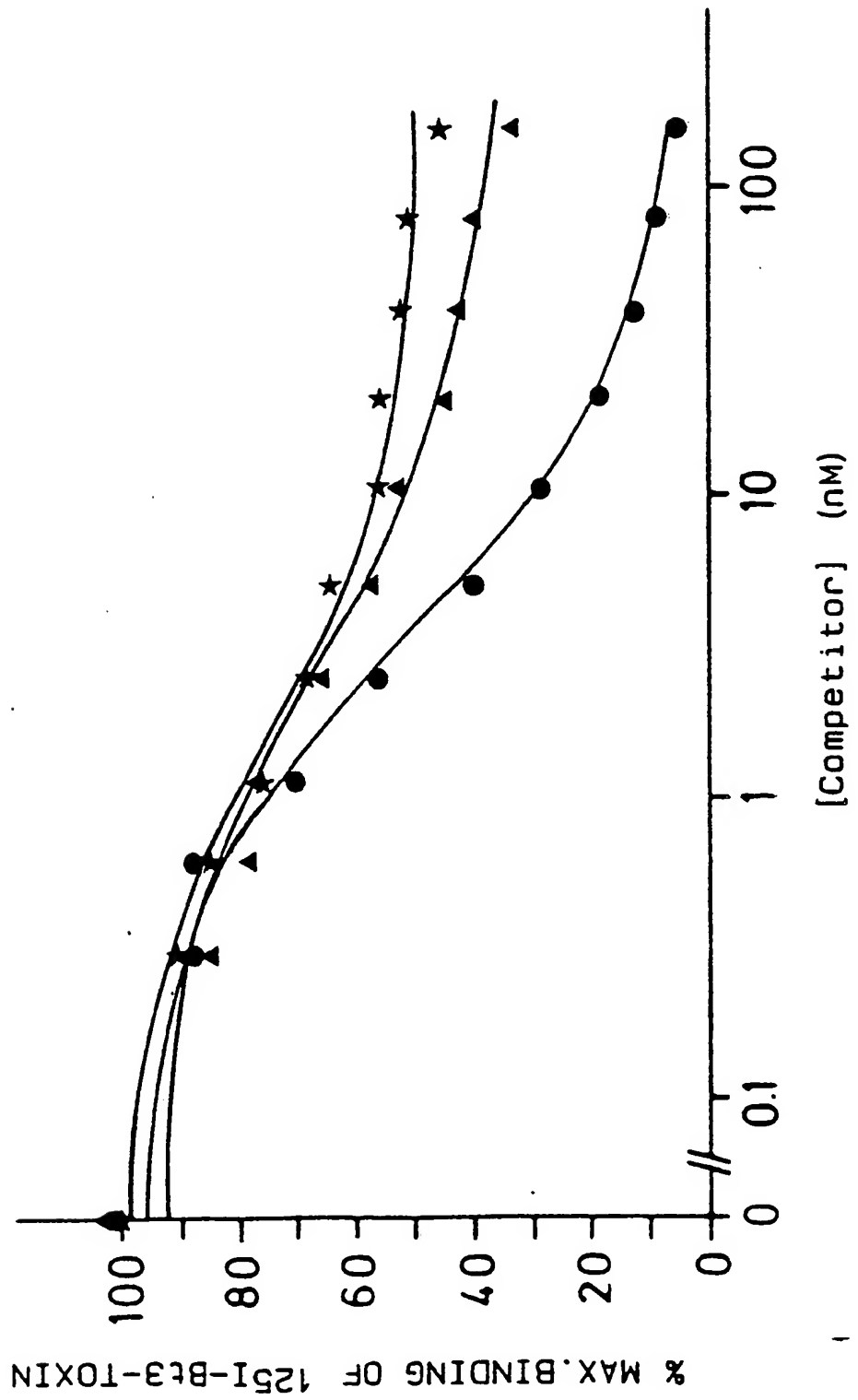


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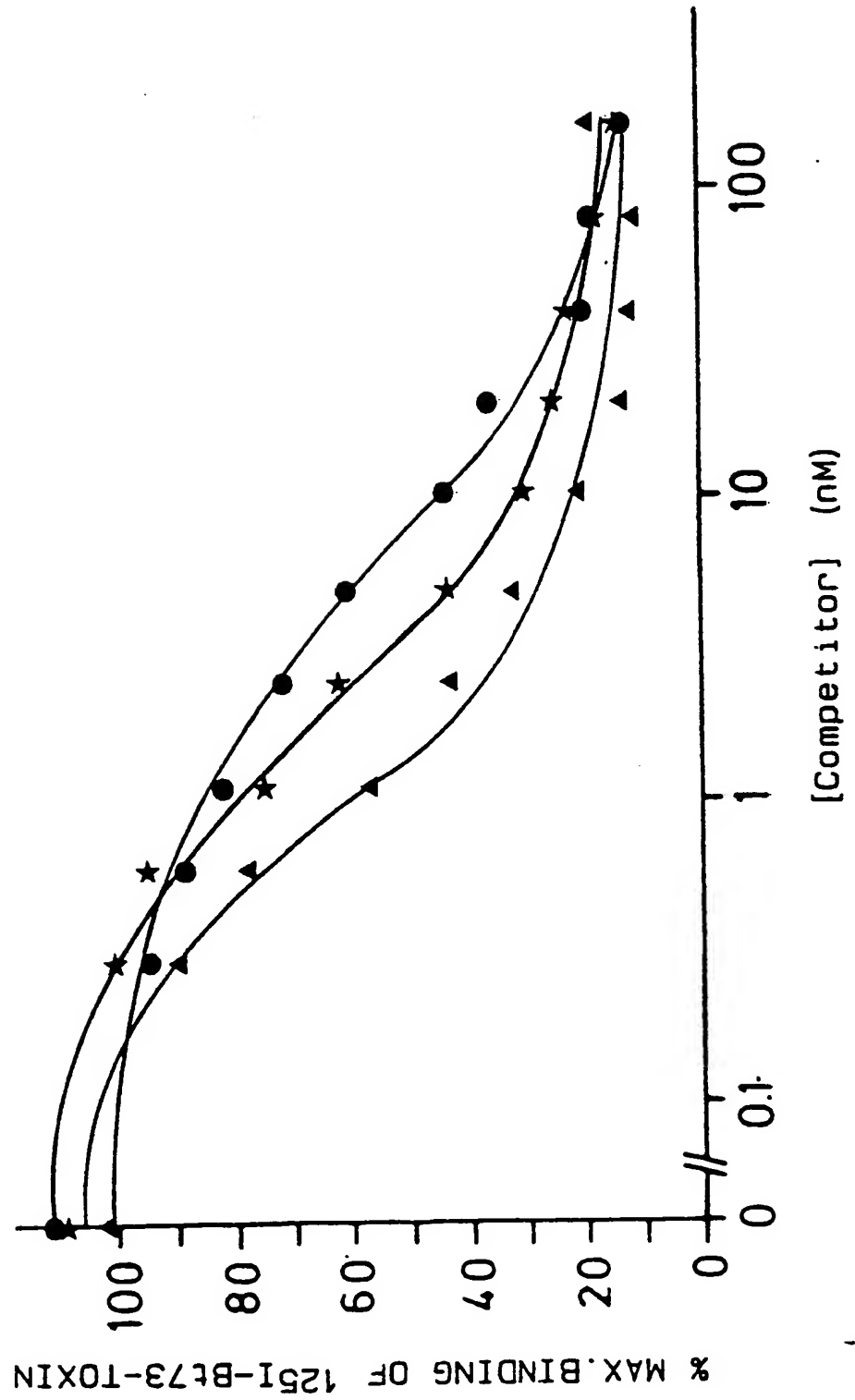


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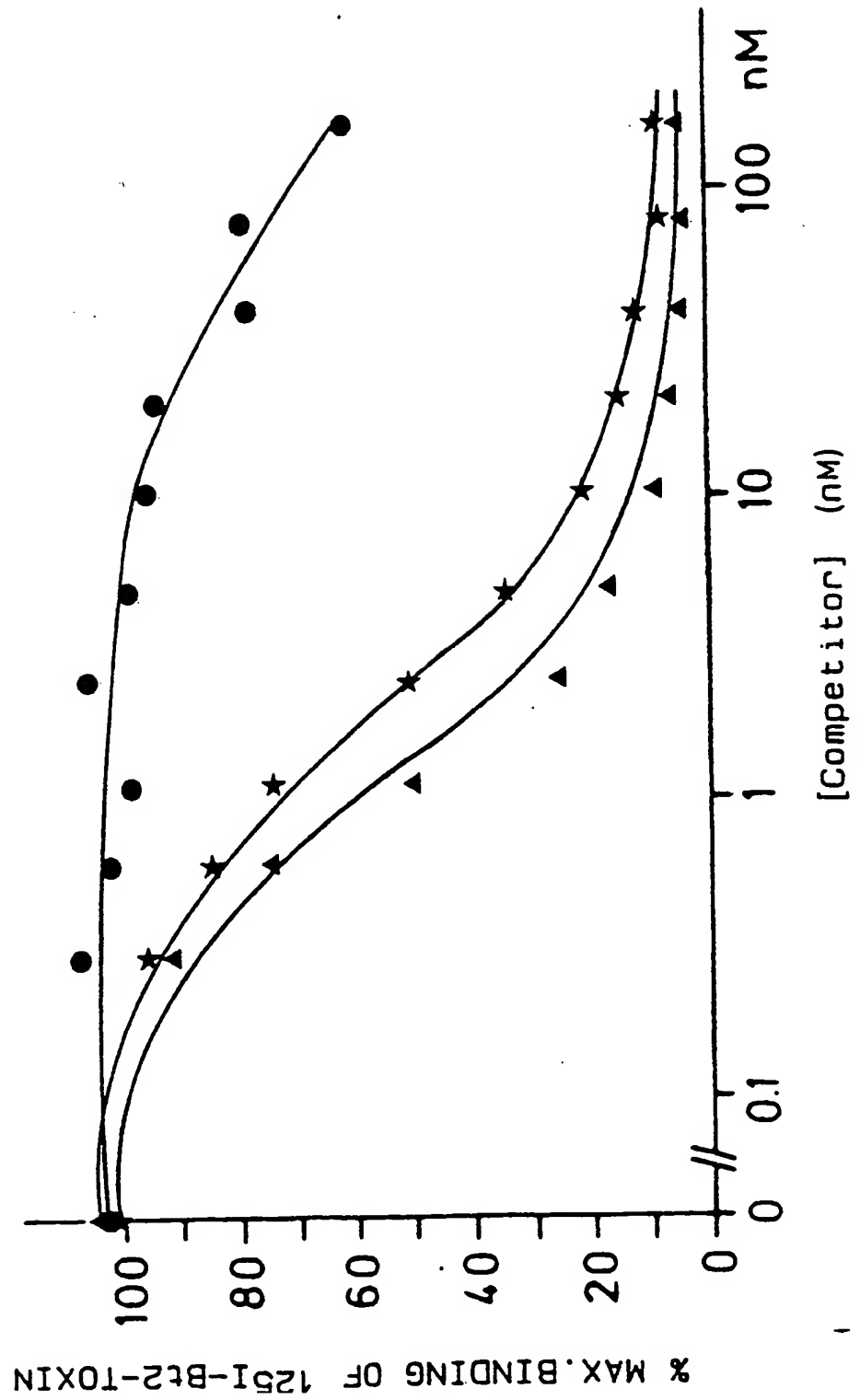


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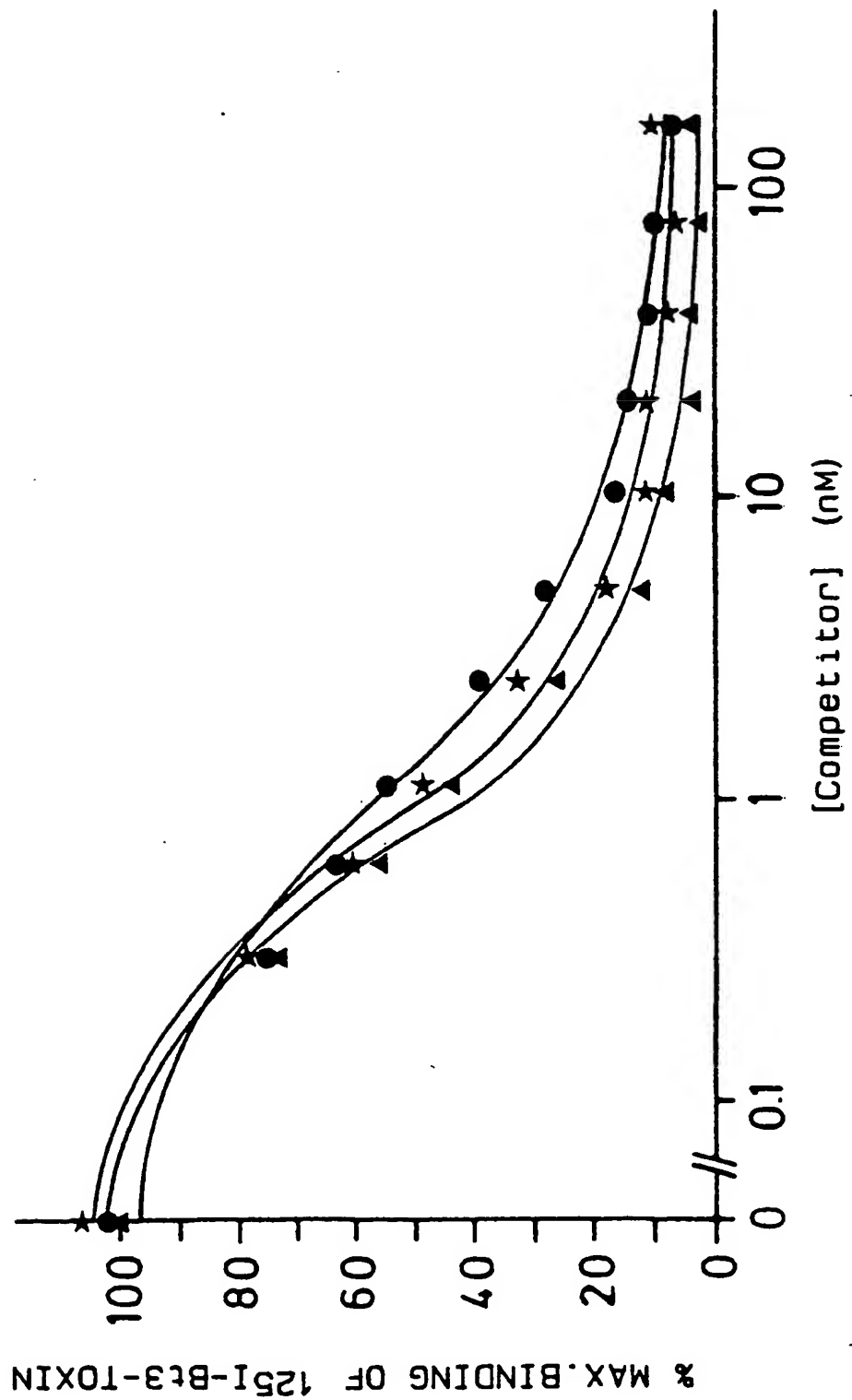


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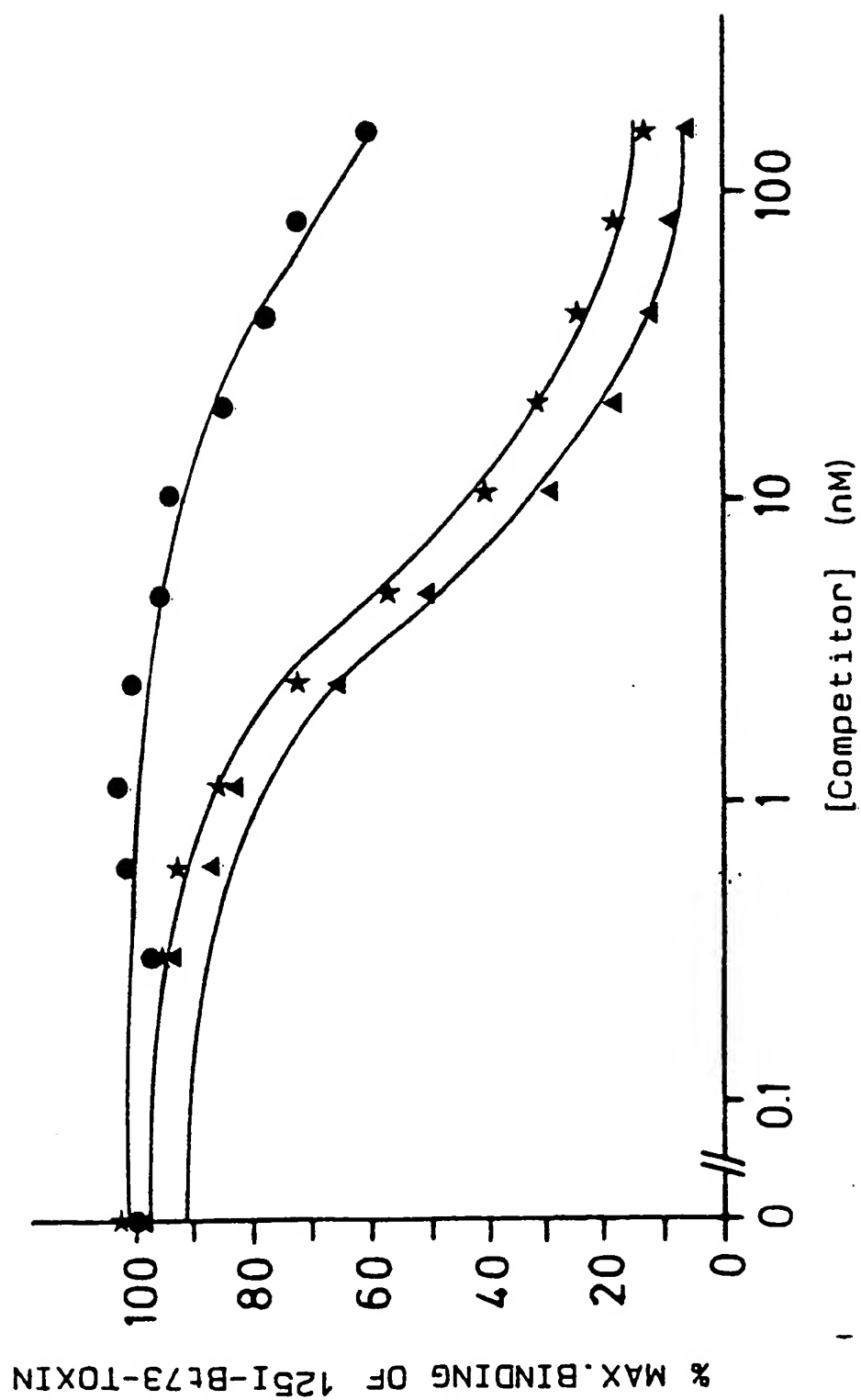


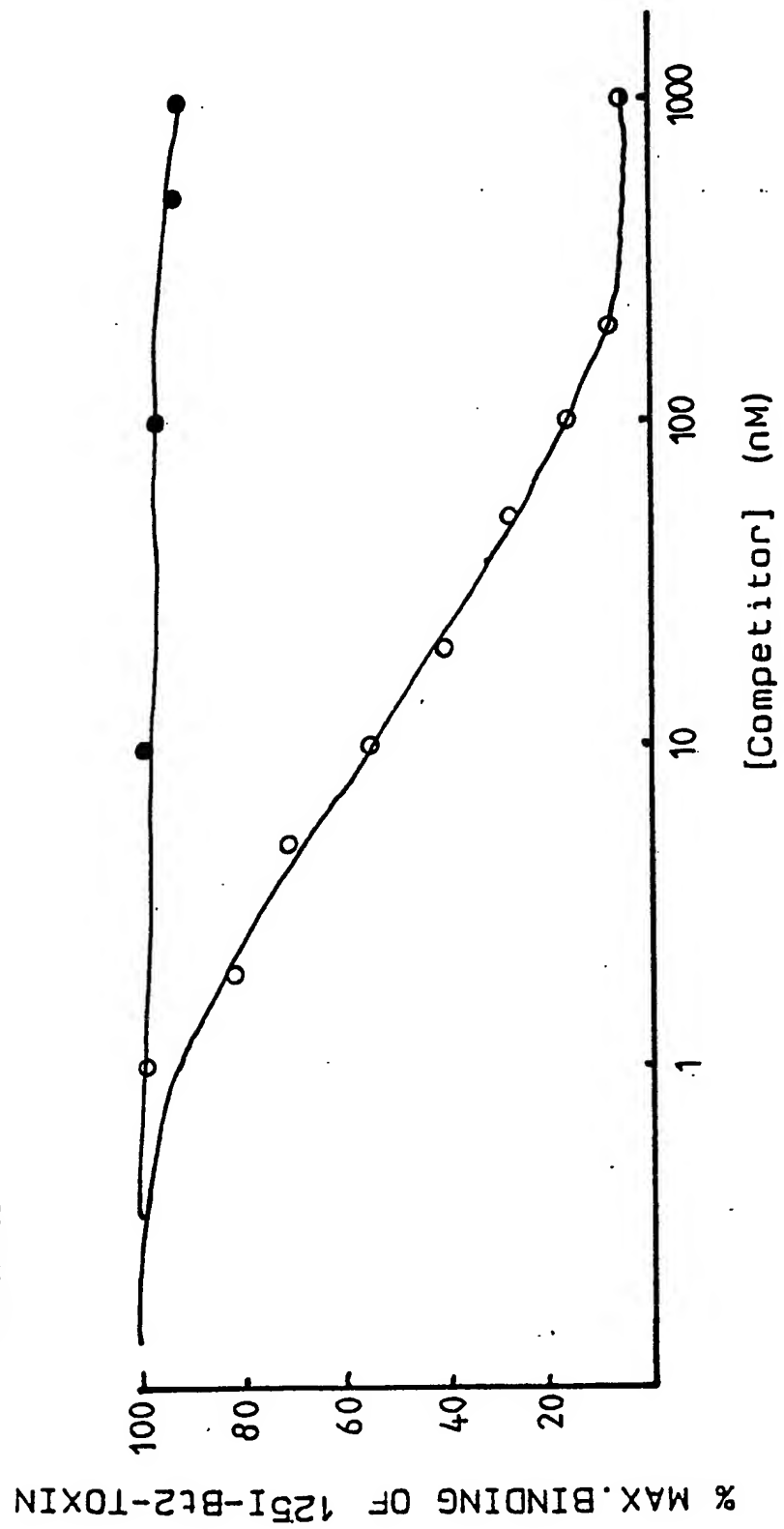
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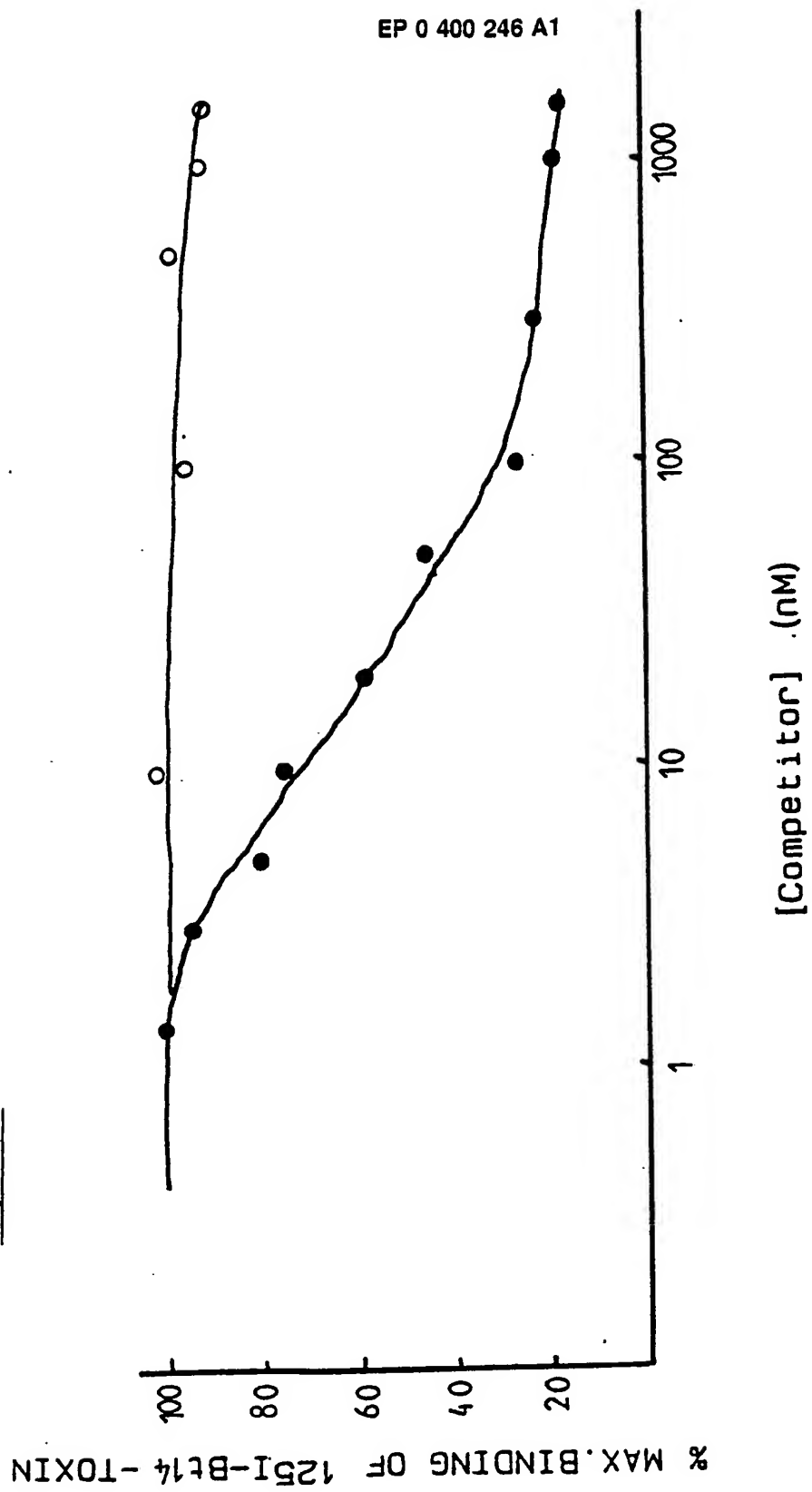
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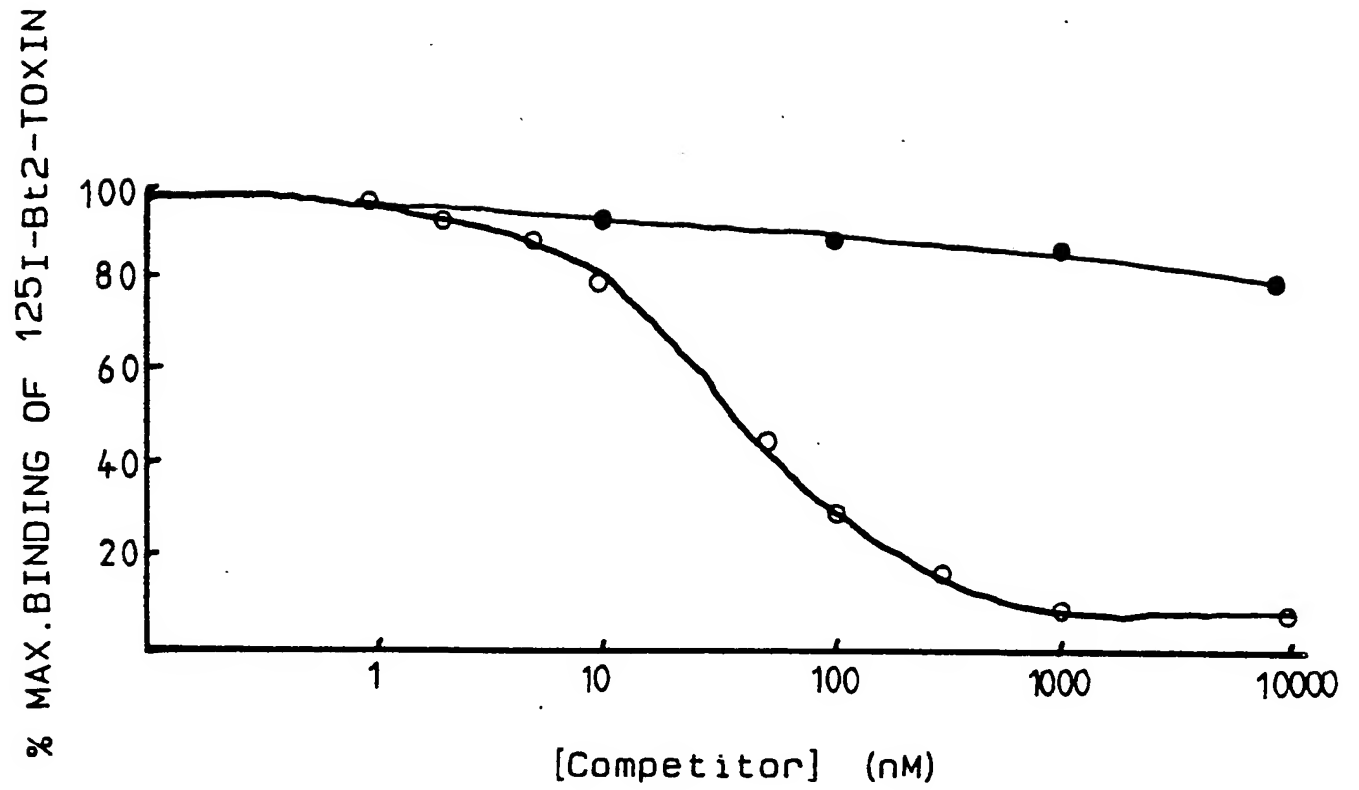
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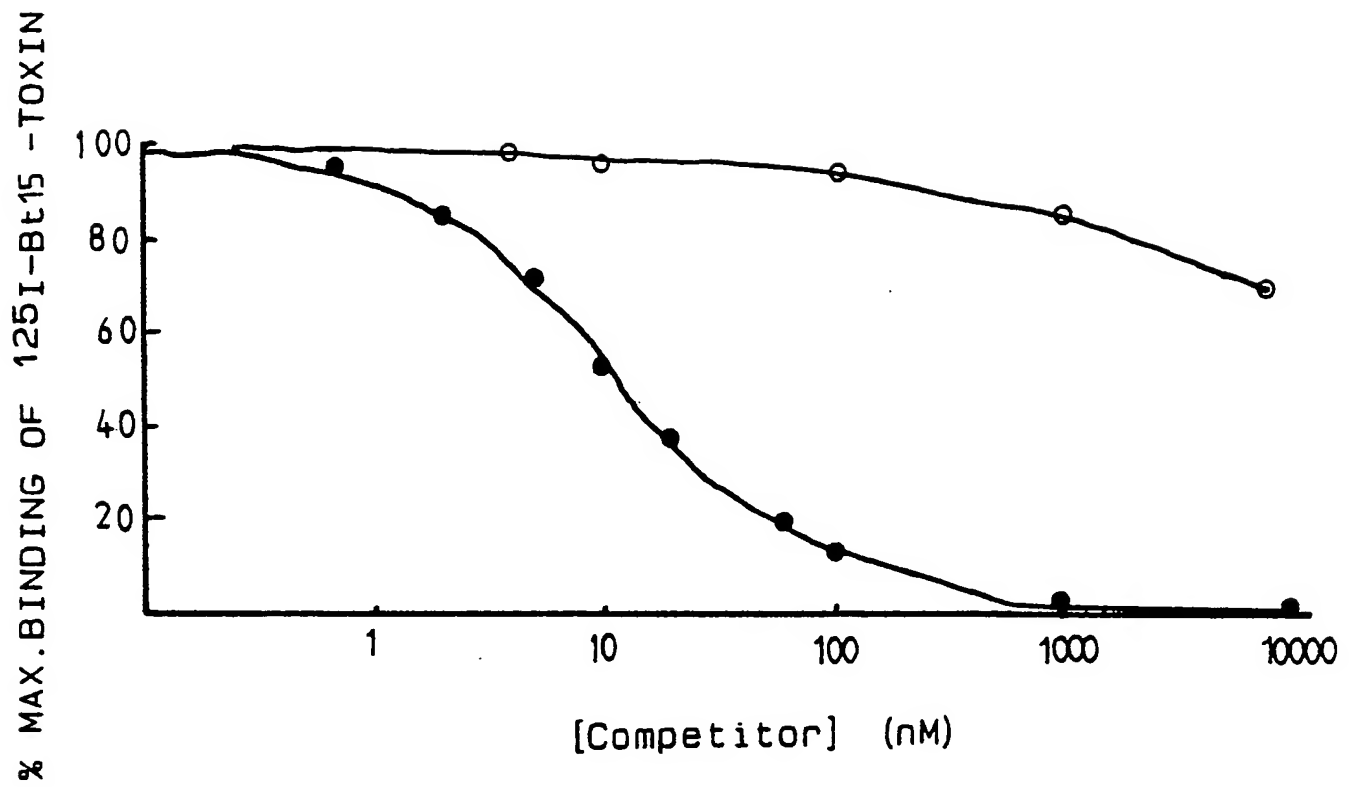
Figure 10

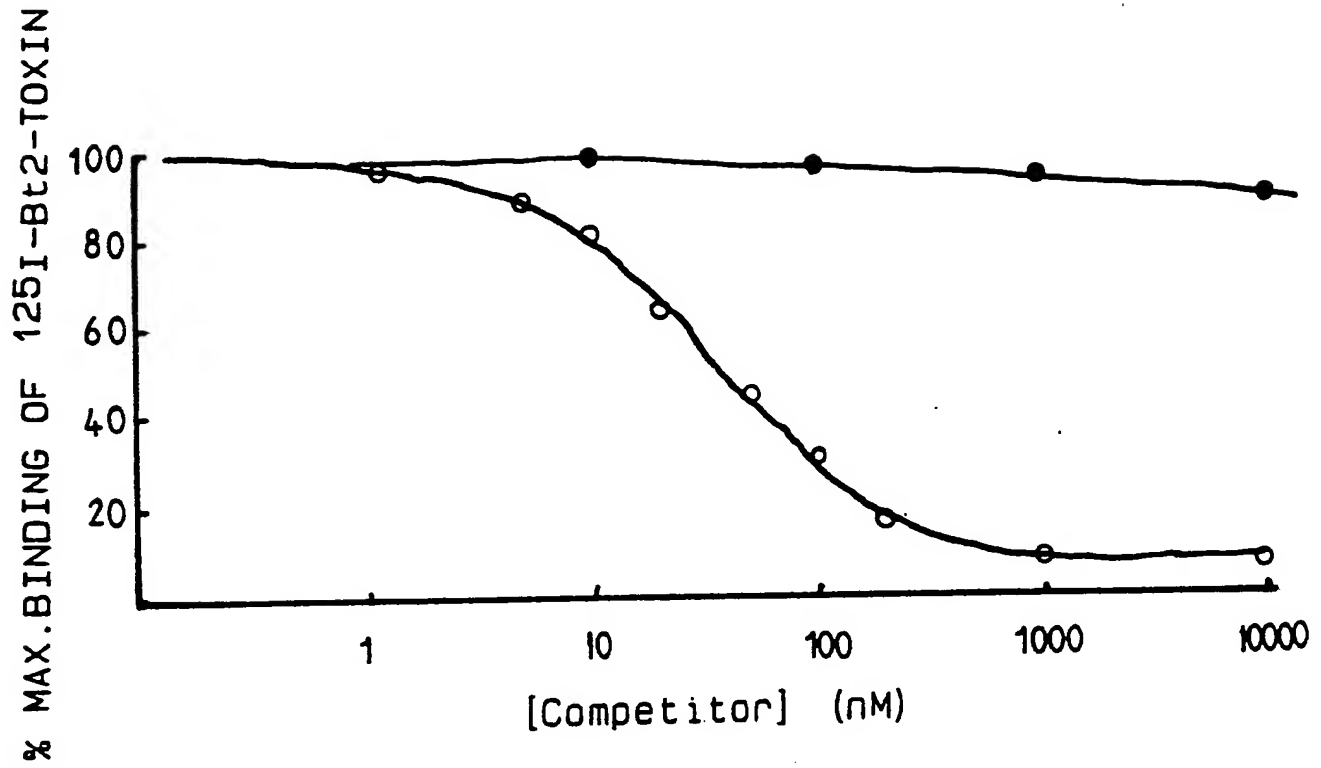
Figure 11

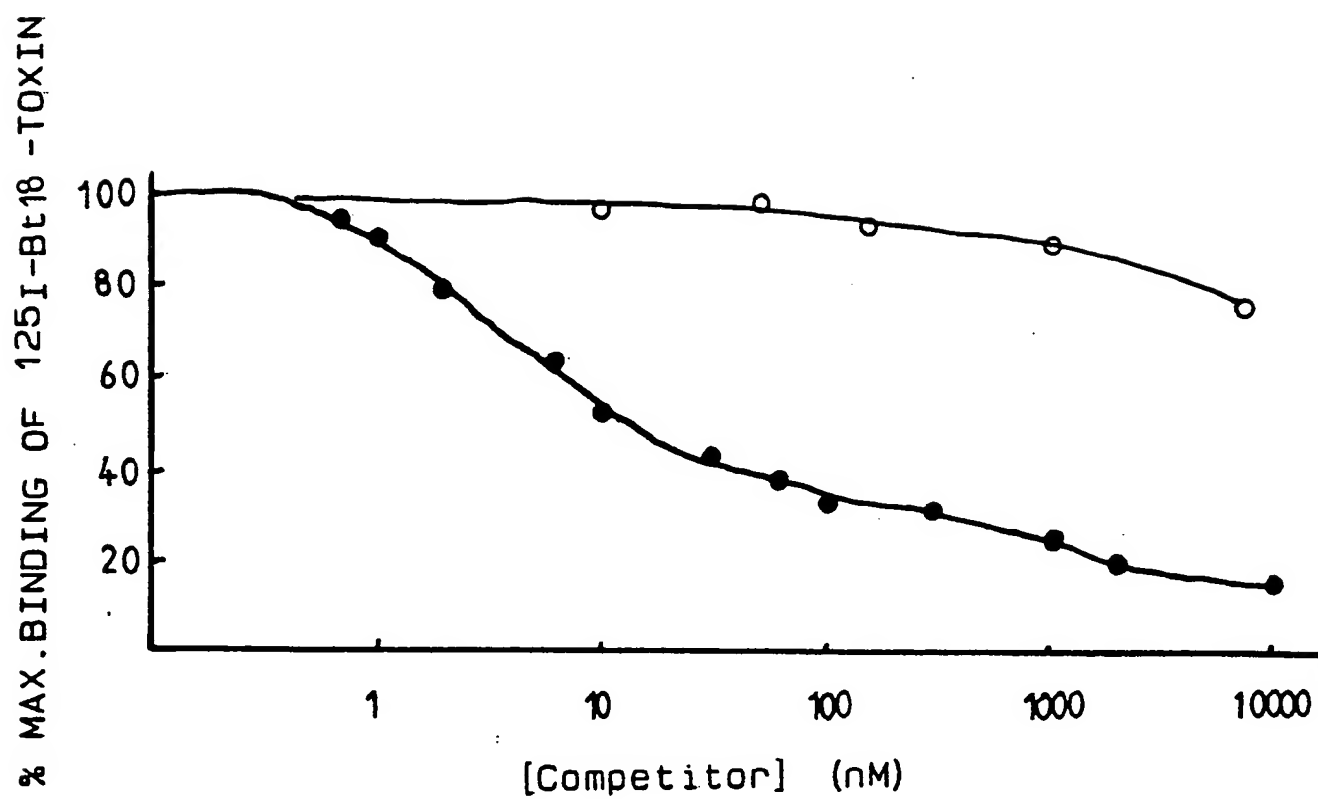
Figure 12

Figure 13

bt4

10	20	30	40	50	60	70
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80	90	100	110	120	130	140
AACTAAATAT	TTTTATAATT	ACACTGATTA	AATACTTTAT	TTTTGGGAGT	AAGATTTATG	CTGAAATGTA
150	160	170	180	190	200	210
ATAAAATTCG	TTCCATTTTC	TGTATTTTCT	CATAAAATGT	TTCATATGCT	TTAAATTGTA	GTAAAGAAAA
220	230	240	250	260	269	
ACAGTACAAA	CTTAAAAGGA	CTTTAGTAAT	TTAATAAAAA	AAGGGGATAG	TTT	$\begin{array}{c} > \\ \overline{ATG} \\ M \end{array}$
						$\begin{array}{c} \overline{GAA} \\ E \end{array}$
						$\begin{array}{c} \overline{ATA} \\ I \end{array}$

AAT AAT CAA AAC CAA TGT GTG CCT TAC AAT TGT TTA AGT AAT CCT AAG GAG ATA
N N Q N Q C V P Y N C L S N P K E I

332 341 350 359 368 377

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I L G E E R L E T G N T V A D I S L

386 395 404 413 422 431

GGG CTT ATT AAT TTT CTA TAT TCT AAT TTT GTA CCA GGA GGA GGA TTT ATA GTA
G L I N F L Y S N F V P G G G F I V

440 449 458 467 476 485

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G L L E L I W G F I G P S Q W D I F

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L A Q I E Q L I S Q R I E E F A R N

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Q A I S R L E G L S N L Y K V Y V R

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D T A T I N N R Y S D L T S L I H V

872 881 890 899 908 917

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Y T N H C V D T Y N Q G L R R L E G

926 935 944 953 962 971

CGT TTT CTT AGC GAT TGG ATT GTA TAT AAT CGT TTC CGG AGA CAA TTG ACA ATT
R F L S D W I V Y N R F R R Q L T I

980 989 998 1007 1016 1025

TCA GTA TTA GAT ATT GTT GCG TTT TTT CCA AAT TAT GAT ATT AGA ACA TAT CCA
S V L D I V A F F P N Y D I R T Y P

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GCT ATA ATT AGA AGT CCT CAT TTA GTA GAC TTT TTA AAT AGC TTT ACC ATT TAT
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3871

3881

3891

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Ile	Val	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile	Glu	Gln	Leu	Ile
491			500			509			518			527			536		
AAT	GAA	AGA	ATA	GCT	GAA	TTT	GCT	AGG	AAT	GCT	GCT	ATT	GCT	AAT	TTA	GAA	GGA
Asn	Glu	Arg	Ile	Ala	Glu	Phe	Ala	Arg	Asn	Ala	Ala	Ile	Ala	Asn	Leu	Glu	Gly
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TTA	GGA	AAC	AAT	TTC	AAT	ATA	TAT	GTG	GAA	GCA	TTT	AAA	GAA	TGG	GAA	GAA	GAT
Leu	Gly	Asn	Asn	Phe	Asn	Ile	Tyr	Val	Glu	Ala	Phe	Lys	Glu	Trp	Glu	Glu	Asp
599			608			617			626			635			644		
CCT	AAT	AAT	CCA	GAA	ACC	AGG	ACC	AGA	GTA	ATT	GAT	CGC	TTT	CGT	ATA	CTT	GAT
Pro	Asn	Asn	Pro	Glu	Thr	Arg	Thr	Arg	Val	Ile	Asp	Arg	Phe	Arg	Ile	Leu	Asp
653			662			671			680			689			698		
GGG	CTA	CTT	GAA	AGG	GAC	ATT	CCT	TCG	TTT	CGA	ATT	TCT	GGA	TTT	GAA	GTA	CCC
Gly	Leu	Leu	Glu	Arg	Asp	Ile	Pro	Ser	Phe	Arg	Ile	Ser	Gly	Phe	Glu	Val	Pro
707			716			725			734			743			752		
CTT	TTA	TCC	GTT	TAT	GCT	CAA	GCG	GCC	AAT	CTG	CAT	CTA	GCT	ATA	TTA	AGA	GAT
Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Ala	Asn	Leu	His	Leu	Ala	Ile	Leu	Arg	Asp
761			770			779			788			797			806		
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Ser	Val	Ile	Phe	Gly	Glu	Arg	Trp	Gly	Leu	Thr	Thr	Ile	Asn	Val	Asn	Glu	Asn
815			824			833			842			851			860		
TAT	AAT	AGA	CTA	ATT	AGG	CAT	ATT	GAT	GAA	TAT	GCT	GAT	CAC	TGT	GCA	AAT	ACG
Tyr	Asn	Arg	Leu	Ile	Arg	His	Ile	Asp	Glu	Tyr	Ala	Asp	His	Cys	Ala	Asn	Thr
869			878			887			896			905			914		
TAT	AAT	CGG	GGA	TTA	AAT	AAT	TTA	CCG	AAA	TCT	ACG	TAT	CAA	GAT	TGG	ATA	ACA
Tyr	Asn	Arg	Gly	Leu	Asn	Asn	Leu	Pro	Lys	Ser	Thr	Tyr	Gln	Asp	Trp	Ile	Thr
923			932			941			950			959			968		
TAT	AAT	CGA	TTA	CGG	AGA	GAC	TTA	ACA	TTG	ACT	GTA	TTA	GAT	ATC	GCC	GCT	TTC
Tyr	Asn	Arg	Leu	Arg	Arg	Asp	Leu	Thr	Leu	Thr	Val	Leu	Asp	Ile	Ala	Ala	Phe
977			986			995			1004			1013			1022		
TTT	CCA	AAC	TAT	GAC	AAT	AGG	AGA	TAT	CCA	ATT	CAG	CCA	GTT	GGT	CAA	CTA	ACA
Phe	Pro	Asn	Tyr	Asp	Asn	Arg	Arg	Tyr	Pro	Ile	Gln	Pro	Val	Gly	Gln	Leu	Thr
1031			1040			1049			1058			1067			1076		
AGG	GAA	GTT	TAT	ACG	GAC	CCA	TTA	ATT	AAT	TTT	AAT	CCA	CAG	TTA	CAG	TCT	GTA
Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Ile	Asn	Phe	Asn	Pro	Gln	Leu	Gln	Ser	Val

GCT	CAA	TTA	CCT	ACT	TTT	AAC	GTT	ATG	GAG	AGC	AGC	GCA	ATT	AGA	AAT	CCT	CAT
Ala	Gln	Leu	Pro	Thr	Phe	Asn	Val	MET	Glu	Ser	Ser	Ala	Ile	Arg	Asn	Pro	His
	1139				1148			1157			1166			1175			1184
TTA	TTT	GAT	ATA	TTG	AAT	AAT	CTT	ACA	ATC	TTT	ACG	GAT	TGG	TTT	AGT	GTT	GGA
Leu	Phe	Asp	Ile	Leu	Asn	Asn	Leu	Thr	Ile	Phe	Thr	Asp	Trp	Phe	Ser	Val	Gly
	1193				1202			1211			1220			1229			1238
CGC	AAT	TTT	TAT	TGG	GGA	GGA	CAT	CGA	GTA	ATA	TCT	AGC	CTT	ATA	GGA	GGT	GGT
Arg	Asn	Phe	Tyr	Trp	Gly	Gly	His	Arg	Val	Ile	Ser	Ser	Leu	Ile	Gly	Gly	Gly
	1247				1256			1265			1274			1283			1292
AAC	ATA	ACA	TCT	CCT	ATA	TAT	GGA	AGA	GAG	GCG	AAC	CAG	GAG	CCT	CCA	AGA	TCC
Asn	Ile	Thr	Ser	Pro	Ile	Tyr	Gly	Arg	Glu	Ala	Asn	Gln	Glu	Pro	Pro	Arg	Ser
	1301				1310			1319			1328			1337			1346
TTT	ACT	TTT	AAT	GGA	CCG	GTA	TTT	AGG	ACT	TTA	TCA	AAT	CCT	ACT	TTA	CGA	TTA
Phe	Thr	Phe	Asn	Gly	Pro	Val	Phe	Arg	Thr	Leu	Ser	Asn	Pro	Thr	Leu	Arg	Leu
	1355				1364			1373			1382			1391			1400
TTA	CAG	CAA	CCT	TGG	CCA	GCG	CCA	CCA	TTT	AAT	TTA	CGT	GGT	GTT	GAA	GGA	GTA
Leu	Gln	Gln	Pro	Trp	Pro	Ala	Pro	Pro	Phe	Asn	Leu	Arg	Gly	Val	Glu	Gly	Val
	1409				1418			1427			1436			1445			1454
GAA	TTT	TCT	ACA	CCT	ACA	AAT	AGC	TTT	ACG	TAT	CGA	GGA	AGA	GGT	ACG	GTT	GAT
Glu	Phe	Ser	Thr	Pro	Thr	Asn	Ser	Phe	Thr	Tyr	Arg	Gly	Arg	Gly	Thr	Val	Asp
	1463				1472			1481			1490			1499			1508
TCT	TTA	ACT	GAA	TTA	CCG	CCT	GAG	GAT	AAT	AGT	GTG	CCA	CCT	CGC	GAA	GGA	TAT
Ser	Leu	Thr	Glu	Leu	Pro	Pro	Glu	Asp	Asn	Ser	Val	Pro	Pro	Arg	Glu	Gly	Tyr
	1517				1526			1535			1544			1553			1562
AGT	CAT	CGT	TTA	TGT	CAT	GCA	ACT	TTT	GTT	CAA	AGA	TCT	GGA	ACA	CCT	TTT	TTA
Ser	His	Arg	Leu	Cys	His	Ala	Thr	Phe	Val	Gln	Arg	Ser	Gly	Thr	Pro	Phe	Leu
	1571				1580			1589			1598			1607			1616
ACA	ACT	GGT	GTA	GTA	TTT	TCT	TGG	ACG	CAT	CGT	AGT	GCA	ACT	CTT	ACA	AAT	ACA
Thr	Thr	Gly	Val	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala	Thr	Leu	Thr	Asn	Thr
	1625				1634			1643			1652			1661			1670
ATT	GAT	CCA	GAG	AGA	ATT	AAT	CAA	ATA	CCT	TTA	GTG	AAA	GGA	TTT	AGA	GTT	TGG
Ile	Asp	Pro	Glu	Arg	Ile	Asn	Gln	Ile	Pro	Leu	Val	Lys	Gly	Phe	Arg	Val	Trp
	1679				1688			1697			1706			1715			1724
GGG	GGC	ACC	TCT	GTC	ATT	ACA	GGA	CCA	GGA	TTT	ACA	GGA	GGG	GAT	ATC	CTT	CGA
Gly	Gly	Thr	Ser	Val	Ile	Thr	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg
	1733				1742			1751			1760			1769			1778
AGA	AAT	ACC	TTT	GGT	GAT	TTT	GTA	TCT	CTA	CAA	GTC	AAT	ATT	AAT	TCA	CCA	ATT
Arg	Asn	Thr	Phe	Gly	Asp	Phe	Val	Ser	Leu	Gln	Val	Asn	Ile	Asn	Ser	Pro	Ile

ACC	CAA	AGA	TAC	CGT	TTA	AGA	TTT	CGT	TAC	GCT	TCC	AGT	AGG	GAT	GCA	CGA	GTT
Thr	Gln	Arg	Tyr	Arg	Leu	Arg	Phe	Arg	Tyr	Ala	Ser	Ser	Arg	Asp	Ala	Arg	Val
	1841			1850			1859			1868			1877			1886	
ATA	GTA	TTA	ACA	GGA	GCG	GCA	TCC	ACA	GGA	GTG	GGA	GGC	CAA	GTT	AGT	GTA	AAT
Ile	Val	Leu	Thr	Gly	Ala	Ala	Ser	Thr	Gly	Val	Gly	Gly	Gln	Val	Ser	Val	Asn
	1895			1904			1913			1922			1931			1940	
ATG	CCT	CTT	CAG	AAA	ACT	ATG	GAA	ATA	GGG	GAG	AAC	TTA	ACA	TCT	AGA	ACA	TTT
MET	Pro	Leu	Gln	Lys	Thr	MET	Glu	Ile	Gly	Glu	Asn	Leu	Thr	Ser	Arg	Thr	Phe
	1949			1958			1967			1976			1985			1994	
AGA	TAT	ACC	GAT	TTT	AGT	AAT	CCT	TTT	TCA	TTT	AGA	GCT	AAT	CCA	GAT	ATA	ATT
Arg	Tyr	Thr	Asp	Phe	Ser	Asn	Pro	Phe	Ser	Phe	Arg	Ala	Asn	Pro	Asp	Ile	Ile
	2003			2012			2021			2030			2039			2048	
GGG	ATA	AGT	GAA	CAA	CCT	CTA	TTT	GGT	GCA	GGT	TCT	ATT	AGT	AGC	GGT	GAA	CTT
Gly	Ile	Ser	Glu	Gln	Pro	Leu	Phe	Gly	Ala	Gly	Ser	Ile	Ser	Ser	Gly	Glu	Leu
	2057			2066			2075			2084			2093			2102	
TAT	ATA	GAT	AAA	ATT	GAA	ATT	ATT	CTA	GCA	GAT	GCA	ACA	TTT	GAA	GCA	GAA	TCT
Tyr	Ile	Asp	Lys	Ile	Glu	Ile	Ile	Leu	Ala	Asp	Ala	Thr	Phe	Glu	Ala	Glu	Ser
	2111			2120			2129			2138			2147			2156	
GAT	TTA	GAA	AGA	GCA	CAA	AAG	GCG	GTG	AAT	GCC	CTG	TTT	ACT	TCT	TCC	AAT	CAA
Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	Asn	Ala	Leu	Phe	Thr	Ser	Ser	Asn	Gln
	2165			2174			2183			2192			2201			2210	
ATC	GGG	TTA	AAA	ACC	GAT	GTG	ACG	GAT	TAT	CAT	ATT	GAT	CAA	GTA	TCC	AAT	TTA
Ile	Gly	Leu	Lys	Thr	Asp	Val	Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu
	2219			2228			2237			2246			2255			2264	
GTG	GAT	TGT	TTA	TCA	GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAG	CGA	GAA	TTG	TCC	GAG
Val	Asp	Cys	Leu	Ser	Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Ser	Glu
	2273			2282			2291			2300			2309			2318	
AAA	GTC	AAA	CAT	GCG	AAG	CGA	CTC	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA
Lys	Val	Lys	His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro
	2327			2336			2345			2354			2363			2372	
AAC	TTC	AGA	GGG	ATC	AAT	AGA	CAA	CCA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACA	GAT
Asn	Phe	Arg	Gly	Ile	Asn	Arg	Gln	Pro	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	Asp
	2381			2390			2399			2408			2417			2426	
ATT	ACC	ATC	CAA	GGA	GGA	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTC	ACA	CTA	CCG
Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	Thr	Leu	Pro
	2435			2444			2453			2462			2471			2480	
GGT	ACC	GTT	GAT	GAG	TGC	TAT	CCA	ACG	TAT	TTA	TAT	CAG	AAA	ATA	GAT	GAG	TCG
Gly	Thr	Val	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	Lys	Ile	Asp	Glu	Ser

AAA	TTA	AAA	GCT	TAT	ACC	CGT	TAT	GAA	TTA	AGA	GGG	TAT	ATC	GAA	GAT	AGT	CAA
Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Glu	Leu	Arg	Gly	Tyr	Ile	Glu	Asp	Ser	Gln
	2543				2552			2561			2570			2579			2588
GAC	TTA	GAA	ATC	TAT	TTG	ATC	CGT	TAC	AAT	GCA	AAA	CAC	GAA	ATA	GTA	AAT	GTG
Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	Asn	Ala	Lys	His	Glu	Ile	Val	Asn	Val
	2597				2606			2615			2624			2633			2642
CCA	GGC	ACG	GGT	TCC	TTA	TGG	CCG	CTT	TCA	GCC	CAA	AGT	CCA	ATC	GGA	AAG	TGT
Pro	Gly	Thr	Gly	Ser	Leu	Trp	Pro	Leu	Ser	Ala	Gln	Ser	Pro	Ile	Gly	Lys	Cys
	2651				2660			2669			2678			2687			2696
GGA	GAA	CCG	AAT	CGA	TGC	GCG	CCA	CAC	CTT	GAA	TGG	AAT	CCT	GAT	CTA	GAT	TGT
Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys
	2705				2714			2723			2732			2741			2750
TCC	TGC	AGA	GAC	GGG	GAA	AAA	TGT	GCA	CAT	CAT	TCC	CAT	CAT	TTC	ACC	TTG	GAT
Ser	Cys	Arg	Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Thr	Leu	Asp
	2759				2768			2777			2786			2795			2804
ATT	GAT	GTT	GGA	TGT	ACA	GAC	TTA	AAT	GAG	GAC	TTA	GGT	GTA	TGG	GTG	ATA	TTC
Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	Phe
	2813				2822			2831			2840			2849			2858
AAG	ATT	AAG	ACG	CAA	GAT	GGC	CAT	GCA	AGA	CTA	GGG	AAT	CTA	GAG	TTT	CTC	GAA
Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu
	2867				2876			2885			2894			2903			2912
GAG	AAA	CCA	TTA	TTA	GGG	GAA	GCA	CTA	GCT	CGT	GTG	AAA	AGA	GCG	GAG	AAG	AAG
Glu	Lys	Pro	Leu	Leu	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys
	2921				2930			2939			2948			2957			2966
TGG	AGA	GAC	AAA	CGA	GAG	AAA	CTG	CAG	TTG	GAA	ACA	AAT	ATT	GTT	TAT	AAA	GAG
Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Asn	Ile	Val	Tyr	Lys	Glu
	2975				2984			2993			3002			3011			3020
GCA	AAA	GAA	TCT	GTA	GAT	GCT	TTA	TTT	GTA	AAC	TCT	CAA	TAT	GAT	AGA	TTA	CAA
Ala	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln
	3029				3038			3047			3056			3065			3074
GTG	GAT	ACG	AAC	ATC	GCG	ATG	ATT	CAT	GCG	GCA	GAT	AAA	CGC	GTT	CAT	AGA	ATC
Val	Asp	Thr	Asn	Ile	Ala	MET	Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Arg	Ile
	3083				3092			3101			3110			3119			3128
CGG	GAA	GCG	TAT	CTG	CCA	GAG	TTG	TCT	GTG	ATT	CCA	GGT	GTC	AAT	GCG	GCC	ATT
Arg	Glu	Ala	Tyr	Leu	Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	Ala	Ala	Ile
	3137				3146			3155			3164			3173			3182
TTC	GAA	GAA	TTA	GAG	GGA	CGT	ATT	TTT	ACA	GCG	TAT	TCC	TTA	TAT	GAT	GCG	AGA
Phe	Glu	Glu	Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Tyr	Ser	Leu	Tyr	Asp	Ala	Arg

AAT	GTC	ATT	AAA	AAT	GGC	GAT	TTC	AAT	AAT	GGC	TTA	TTA	TGC	TGG	AAC	GTG	AAA
Asn	Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	Leu	Leu	Cys	Trp	Asn	Val	Lys

3245	3254	3263	3272	3281	3290
------	------	------	------	------	------

GGT	CAT	GTA	GAT	GTA	GAA	GAG	CAA	AAC	AAC	CAC	CGT	TCG	GTC	CTT	GTT	ATC	CCA
Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn	Asn	His	Arg	Ser	Val	Leu	Val	Ile	Pro

3299	3308	3317	3326	3335	3344
------	------	------	------	------	------

GAA	TGG	GAG	GCA	GAA	GTG	TCA	CAA	GAG	GTT	CGT	GTC	TGT	CCA	GGT	CGT	GGC	TAT
Glu	Trp	Glu	Ala	Glu	Val	Ser	Gln	Glu	Val	Arg	Val	Cys	Pro	Gly	Arg	Gly	Tyr

3353	3362	3371	3380	3389	3398
------	------	------	------	------	------

ATC	CTT	CGT	GTC	ACA	GCA	TAT	AAA	GAG	GGG	TAT	GGG	GAG	GGC	TGC	GTA	ACG	ATC
Ile	Leu	Arg	Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile

3407	3416	3425	3434	3443	3452
------	------	------	------	------	------

CAT	GAG	ATC	GAA	GAC	AAT	ACA	GAC	GAA	CTG	AAA	TTC	AGC	AAC	TGT	GTA	GAA	GAG
His	Glu	Ile	Glu	Asp	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Ser	Asn	Cys	Val	Glu	Glu

3461	3470	3479	3488	3497	3506
------	------	------	------	------	------

GAA	GTA	TAT	CCA	AAC	AAC	ACA	GTA	ACG	TGT	AAT	AAT	TAT	ACT	GGG	ACT	CAA	GAA
Glu	Val	Tyr	Pro	Asn	Asn	Thr	Val	Thr	Cys	Asn	Asn	Tyr	Thr	Gly	Thr	Gln	Glu

3515	3524	3533	3542	3551	3560
------	------	------	------	------	------

GAA	TAT	GAG	GGT	ACG	TAC	ACT	TCT	CGT	AAT	CAA	GGA	TAT	GAC	GAA	GCC	TAT	GGT
Glu	Tyr	Glu	Gly	Thr	Tyr	Thr	Ser	Arg	Asn	Gln	Gly	Tyr	Asp	Glu	Ala	Tyr	Gly

3569	3578	3587	3596	3605	3614
------	------	------	------	------	------

AAT	AAC	CCT	TCC	GTA	CCA	GCT	GAT	TAC	GCT	TCA	GTC	TAT	GAA	GAA	AAA	TCG	TAT
Asn	Asn	Pro	Ser	Val	Pro	Ala	Asp	Tyr	Ala	Ser	Val	Tyr	Glu	Glu	Lys	Ser	Tyr

3623	3632	3641	3650	3659	3668
------	------	------	------	------	------

ACA	GAT	GGA	CGA	AGA	GAG	AAT	CCT	TGT	GAA	TCT	AAC	AGA	GGC	TAT	GGG	GAT	TAC
Thr	Asp	Gly	Arg	Arg	Glu	Asn	Pro	Cys	Glu	Ser	Asn	Arg	Gly	Tyr	Gly	Asp	Tyr

3677	3686	3695	3704	3713	3722
------	------	------	------	------	------

ACA	CCA	CTA	CCG	GCT	GGT	TAT	GTA	ACA	AAG	GAT	TTA	GAG	TAC	TTC	CCA	GAG	ACC
Thr	Pro	Leu	Pro	Ala	Gly	Tyr	Val	Thr	Lys	Asp	Leu	Glu	Tyr	Phe	Pro	Glu	Thr

3731	3740	3749	3758	3767	3776
------	------	------	------	------	------

GAT	AAG	GTA	TGG	ATT	GAG	ATC	GGG	GAA	ACA	GAA	GGA	ACA	TTC	ATC	GTG	GAT	AGC
Asp	Lys	Val	Trp	Ile	Glu	Ile	Gly	Glu	Thr	Glu	Gly	Thr	Phe	Ile	Val	Asp	Ser

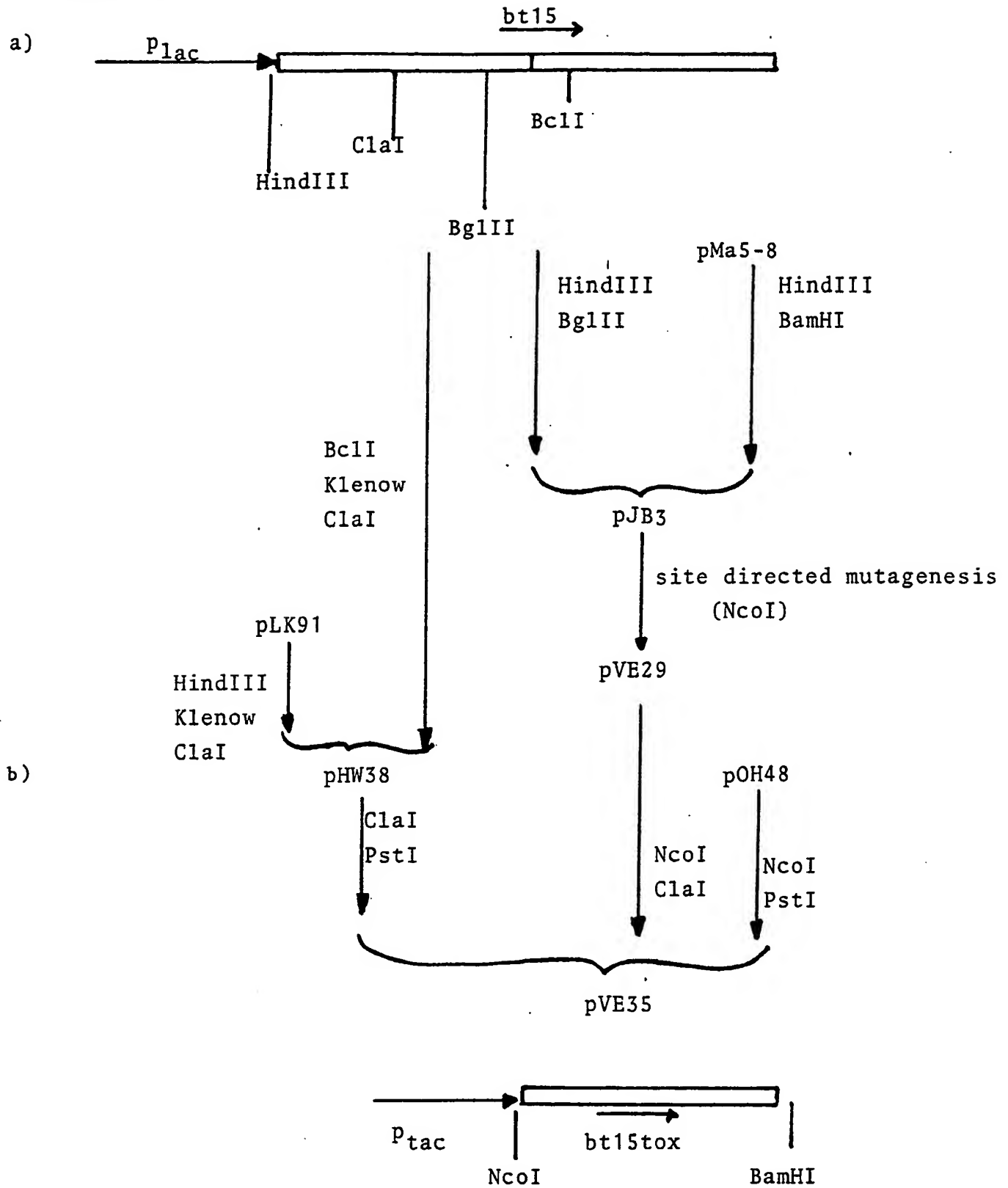
3785	3794	3803	3813	3823	3833
------	------	------	------	------	------

GTG	GAA	TTA	CTC	CTT	ATG	GAG	GAA	TAA	>								
Val	Glu	Leu	Leu	Leu	MET	Glu	Glu	Glu	GATACGTTAT AAAATGTAAC GTATGCAAAT								

3843	3853	3863	3873	3883	3893	3903
------	------	------	------	------	------	------

AAAGAATGAT TACTGACCTA TATTAACAGA TAAATAAGAA AATTTTTATA CGAATAAAAA ACGGACATCA

Figure 15



c)

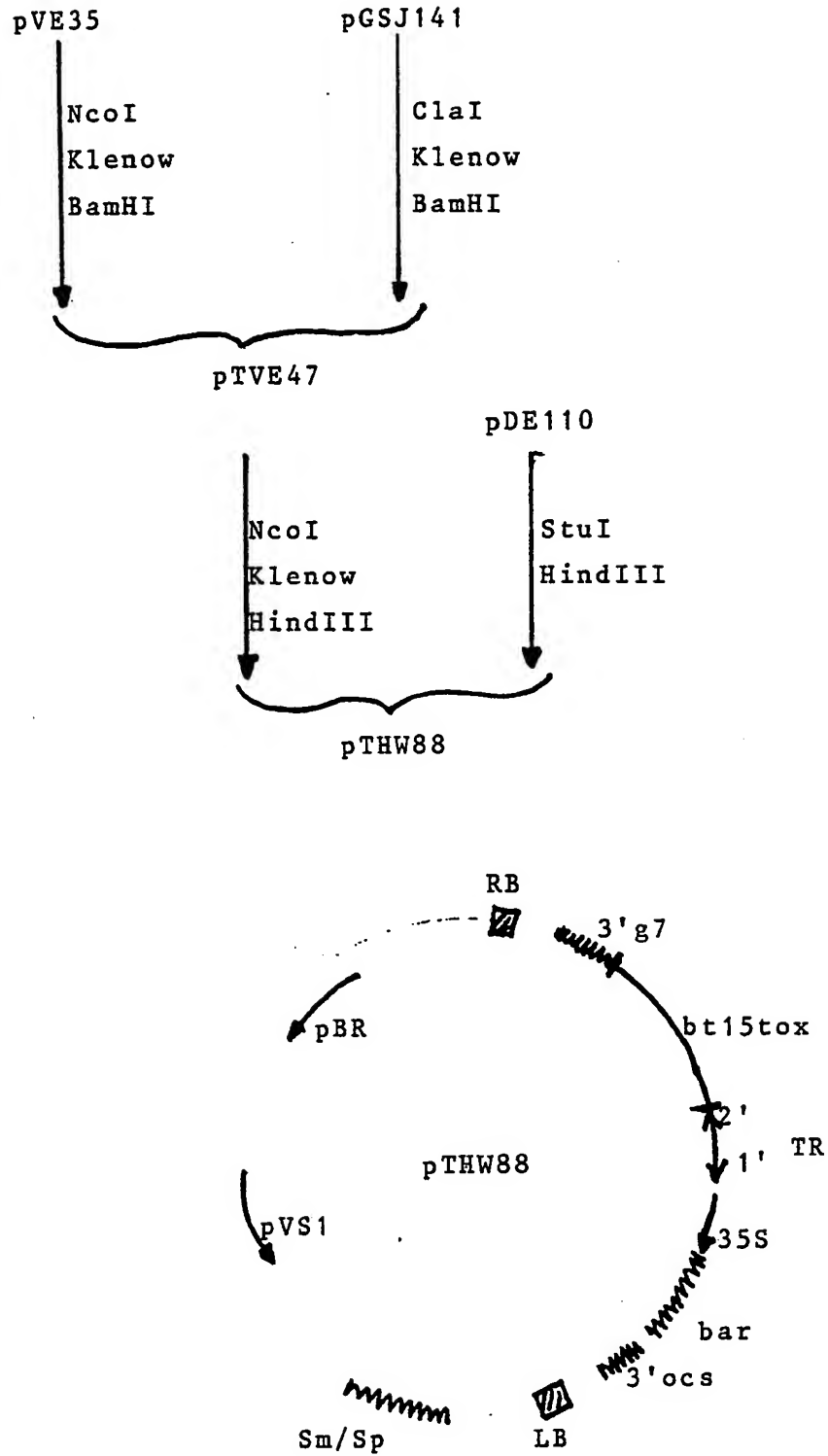
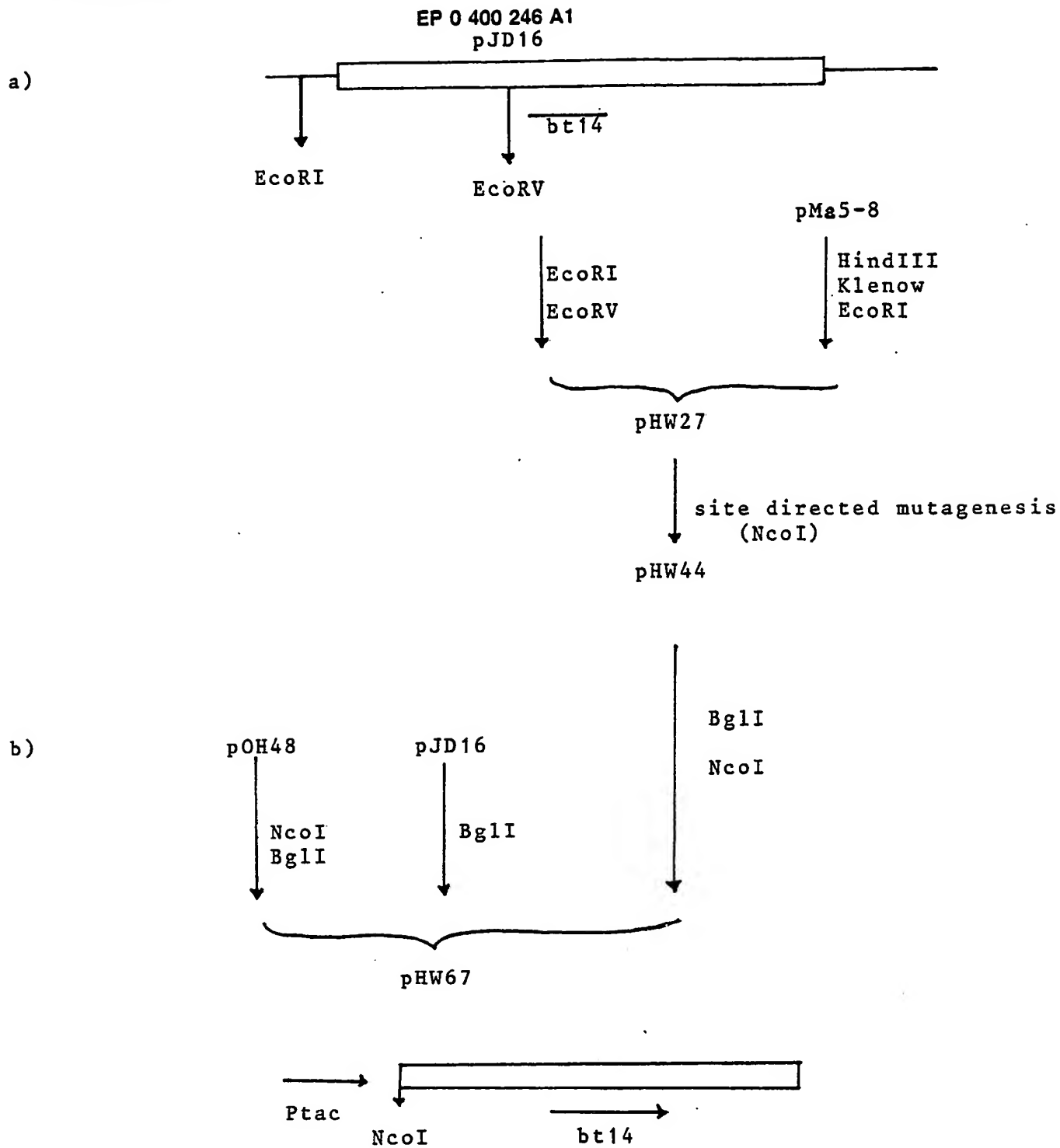
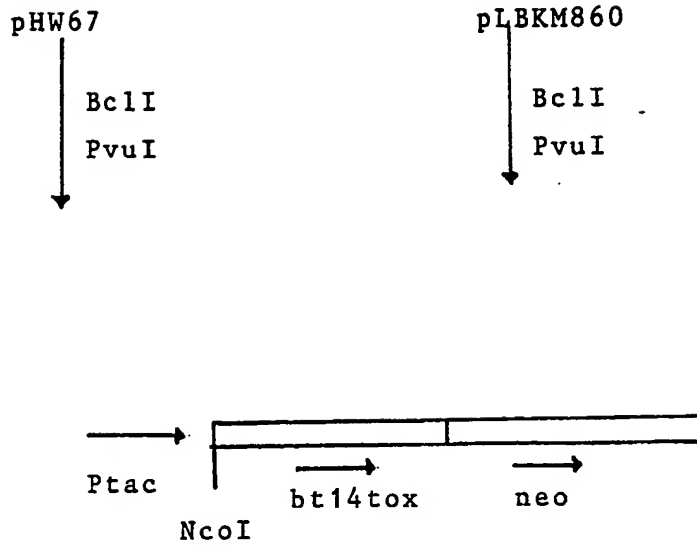


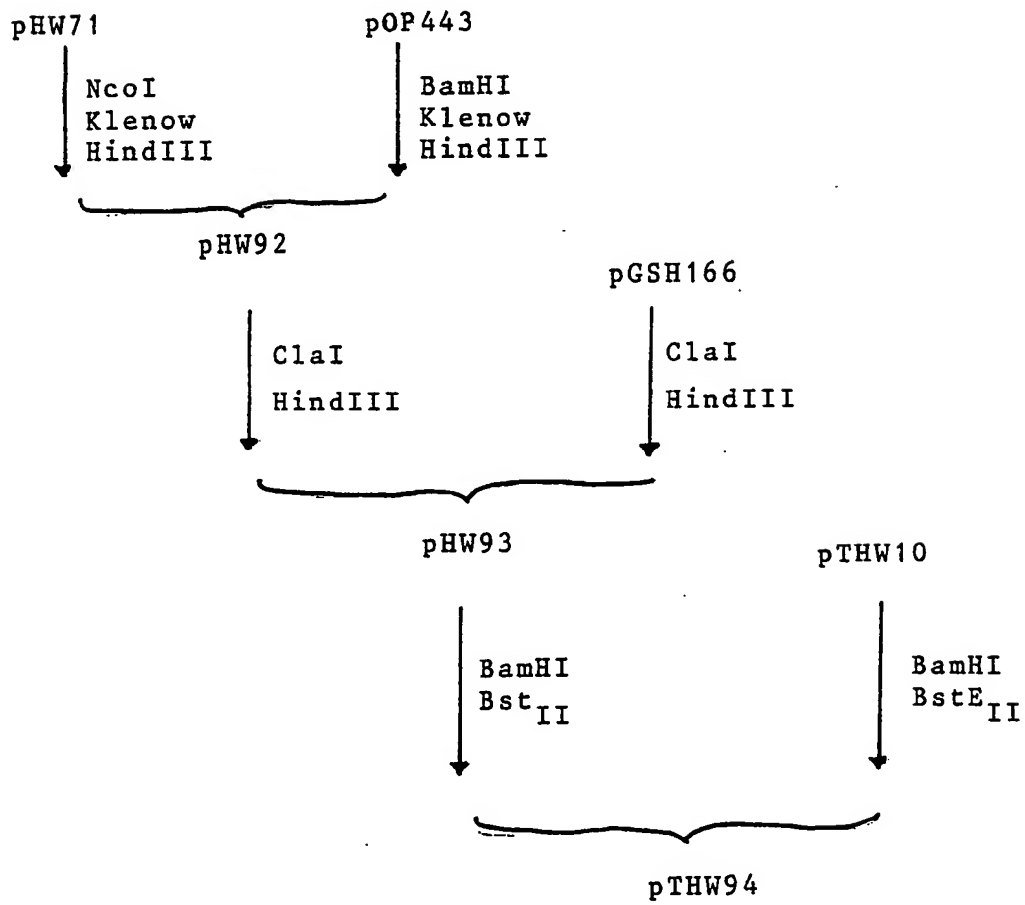
FIG 15 - END -



c)



d)



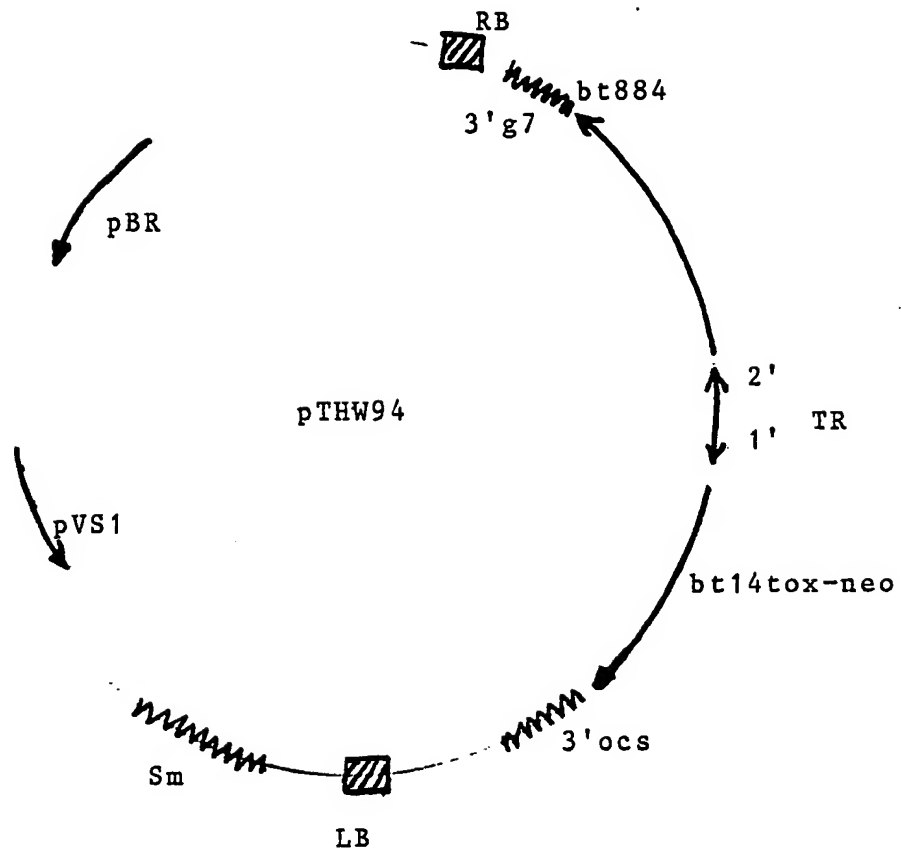
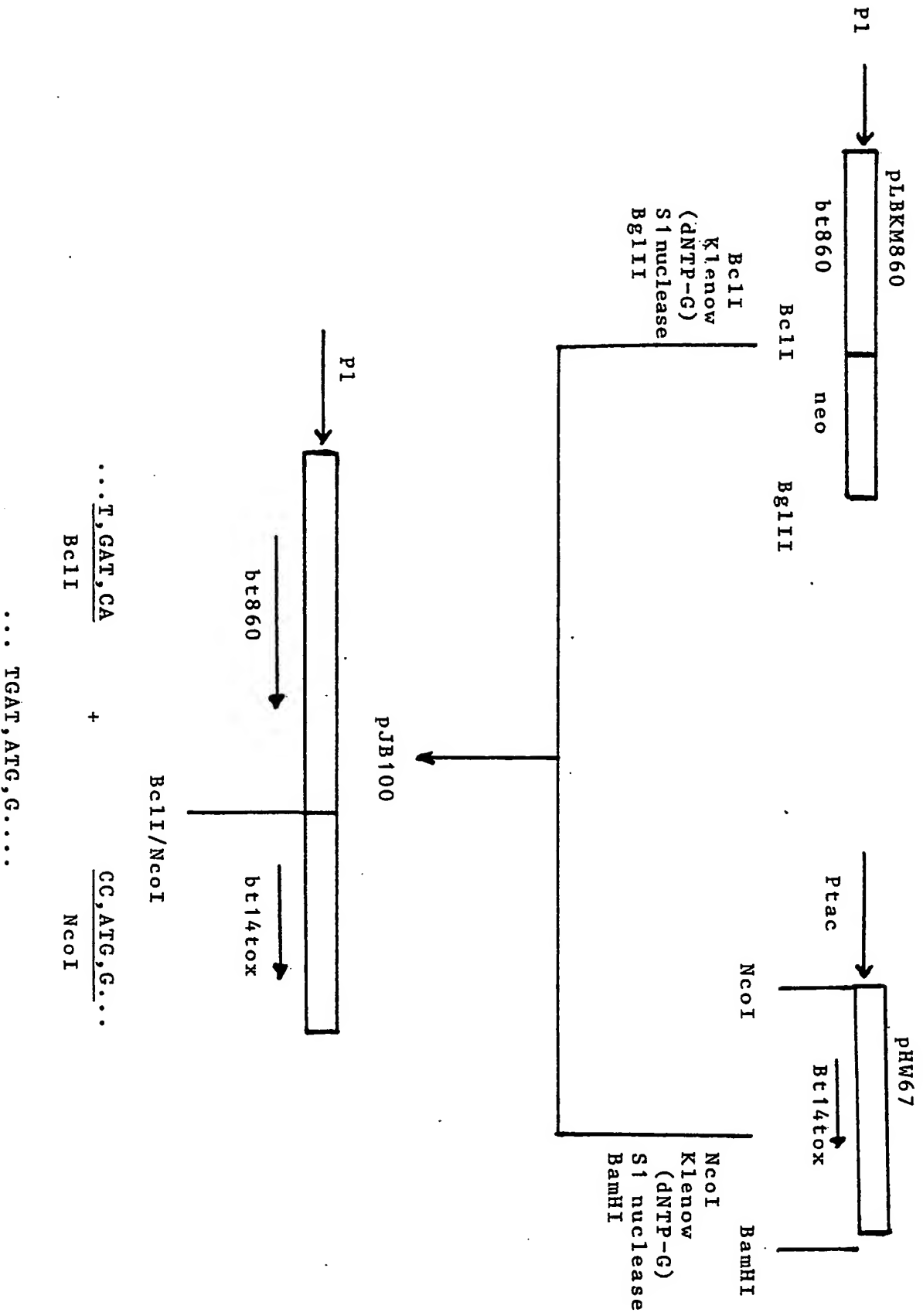


FIG 16-END-

Figure 17





DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl.5)
Y	EP-A-0 228 838 (MYCOGEN CORP.) * whole document; in particular page 7, example 5 * ---	1,13-16 ,27,29	C 12 N 15/32 A 01 N 63/00
Y	WO-A-8 808 880 (ECOGEN, INC.) * abstract; page 11, line 18 - page 13, line 12; page 25, line 9 - page 27, line 15; page 41, line 33 - page 42, line 28; claims * ---	1,13-16 ,27,29	
D,A	EP-A-0 193 259 (PLANT GENETIC SYSTEMS N.V.) * whole document * ---	1,13-16 ,27,29	
Y	EP-A-0 192 319 (MYCOGEN CORP.) * whole document; in particular page 6, lines 20-24 * ---	1	
Y	EP-A-0 221 024 (SANDOZ AG) * whole document; in particular page 3, lines 30-34 * ---	1	
A	PATENT ABSTRACTS OF JAPAN vol. 12, no. 391 (C537)(3238), 18 October 1988; & JP - A - 63 137684 (SUMITOMO CHEM. CO. LTD.) 09.06.1988 -----	1	
The present search report has been drawn up for all claims			
Place of search BERLIN		Date of completion of the search 18-10-1989	Examiner JULIA P.
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons ----- & : member of the same patent family, corresponding document			